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(71) Applicant *(for all designated States except US)*: ZENECA LIMITED [GB/GB]; 15 Stanhope Gate, London W1Y 6LN (GB).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: COPLEY, Clive, Graham [GB/GB]; Zeneca Pharmaceuticals, Mereside, Alderley Park, Macclesfield, Cheshire SK10 4TG (GB). EDGE, Michael, Derek [GB/GB]; Zeneca Pharmaceuticals, Mereside, Alderley Park, Macclesfield, Cheshire SK10 4TG (GB). EMERY, Stephen, Charles [GB/GB]; Zeneca Pharmaceuticals, Mereside, Alderley Park, Macclesfield, Cheshire SK10 4TG (GB).

(74) Agent: GILES, Allen, Frank; Zeneca Pharmaceuticals, Intellectual Property Dept., Mereside, Alderley Park, Macclesfield, Cheshire SK10 4TG (GB).

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(54) Title: MONOCLONAL ANTIBODY TO CEA, CONJUGATES COMPRISING SAID ANTIBODY, AND THEIR THERAPEUTIC USE IN AN ADEPT SYSTEM

(57) Abstract

The invention relates to an anti-CEA monoclonal antibody (named "806.077 antibody") of murine origin and useful for the diagnosis and therapy of cancer. The antibody complementarity determining regions (CDRs) have the following sequences: heavy chain; CDR1 DNYMH, CDR2 WIDPENGDTE YAPKFRG, CDR3 LIYAGYLAMD Y; and light chain CDR1 SASSSVTYMH, CDR2 STSNLAS, CDR3 QQRSTYPLT. Humanised antibodies are described. The antibody is preferably in the form of a conjugate with either an enzyme suitable for use in an ADEPT system, especially a carboxypeptidase, or with a co-stimulatory molecule such as the extracellular domain of human B7.1.

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MONOCLONAL ANTIBODY TO CEA, CONJUGATES COMPRISING SAID ANTIBODY, AND THEIR THERAPEUTIC USE IN AN ADEPT SYSTEM

The present invention relates to a novel anti-CEA monoclonal antibody (named "806.077 antibody" or "806.077 Ab" herein) useful for the diagnosis and therapy of cancer.

It is established that the transformation of normal tissue cells to tumour cells is associated with a change in structure on the cell surface. Altered cell surface structures can serve as antigens and the tumour modified structures represent a type of so-called tumour-associated antigen (see for example Altered Glycosylation in Tumour Cells, Eds. Reading, Hakamori and Marcus 1988, Arthur R. Liss publ.). Such antigens may be exploited for example by the generation of monospecific antibodies using hybridoma technology as is presently well established after being first described by Kohler and Milstein (Nature, 256, 495-497, 1975).

One tumour-associated antigen is CEA (Carcinomembryonic Antigen) as first described by Gold and Freedman, J Exp Med, 121, 439, 1965. This antigen is present on the tumour cell surface and can also be demonstrated in blood serum.

The concept of using antibodies to target tumour associated antigens in the treatment of cancer has been appreciated for some time (Herlyn et.al. (1980) Cancer Research 40, 717). Antibodies may be used to target various chemical and biological agents to the tumour and such conjugates have been particularly successful in forming the basis for many methods of both in vitro and in vivo diagnosis. The use of immunoconjugates in the therapy of cancer is also promising (Lord et al.(1985) Trends in Biotechnology 3, 175; Vitetta et al (1987) Science 238, 1098). This approach is technically more demanding than diagnostic applications and requires that tumour associated antigens which are targetted in such immunotherapeutic approaches, are highly tumour specific and not expressed at significant levels in vital human tissues. Whilst not wishing to be bound by theoretical considerations, as well as the property of having specific tumour associated tissue distribution, for some applications it is desirable that the antibody remain at the cell surface after antigen binding rather than being quickly internalised. For example in ADEPT (antibody directed enzyme prodrug therapy, see US patents 4975278 and 5405990) it is believed to be preferred that the antibody remain at the cell surface to facilitate prodrug activation by antibody-enzyme conjugate.

Antibody conjugates also have application in tumour immunotherapy. The following few paragraphs set out the scientific background for this application. In order to respond to an

immune stimulus, T-cells require two signals. One such signal is provided by recognition of MHC displayed peptides by the T-cell receptor (TCR). It has been demonstrated however that TCR stimulation alone results in T-cell unresponsiveness or anergy and a second or co-stimulatory signal is required to stimulate specific T-cell activation and proliferation (reviewed by Schwartz R.H. J.Exp.Med., 1996, 184, 1-8). Upon receiving both signals, the resulting cytotoxic T-cells mediate the immune response by killing the target cells. A number of potential co-stimulatory molecules have been identified (eg B7, ICAMs, LFA-1 and 3, CD40, CD70 and CD24, reviewed by Galea-Lauri J. *et al* Cancer Gene Therapy, 1996, 3, 202-213). The major co-stimulatory function appears to be provided by the related molecules B7.1 (also called CD80) and B7.2 (also called CD86) which can interact with two receptors, CD28 and CTLA-4 (Hellstrom K.E. *et al* Immunol. Rev., 1995, 145, 123-145 and Lenschow D.J. *et al* Ann.Rev.Immunol., 1996, 14, 233-258). B7.1 and B7.2 are expressed on antigen presenting cells (APC) such as dendritic cells whereas CD28 and CTLA-4 are present on T-cells. B7.2 appears to be constitutively expressed on the surface of APCs but after contact with a T-cell, expression of B7.1 is up-regulated. Analogously, CD28 is expressed on T-cells but after activation is down-regulated and replaced by CTLA-4 expression. The stimulation of CD28 and CTLA-4 by B7.1 and B7.2 represents a complex pattern of signalling which controls not only the activation of the T-cell, but the subsequent control of proliferation to modulate the immune-response (Greene J. *et al* J.Biol.Chem., 1996, 271, 26762-26771). This phenomenon may explain the sometimes conflicting data reported by workers studying these co-stimulatory molecules.

In cancer, tumour infiltrating lymphocytes have been identified but the lack of immune-response to the tumour may be due to T-cell anergy. Tumour cells can display specific or selective antigens on their surface but lack B7.1/B7.2 allowing them to escape immune surveillance. Indeed, *in vivo* experiments have demonstrated that B7.1/B7.2 transfected tumour cells are less tumourigenic than untransfected cells from the same line and that the transfected cells are capable of inducing protective immunity against rechallenge with parental cells (Townsend S.E. and Allison J.P., 1993, Science, 259, 368-370). This demonstrates that once stimulated, the immune response can become B7.1/B7.2 independent. Hellstrom has proposed that expression of B7.1/B7.2 in tumour cells by gene therapy has the potential to stimulate a host reponse which can reduce or eliminate the disease. Gajewski (J.Immunol., 1996, 156, 465-472) and Matulonis *et al* (J.Immunol., 1996, 156, 1126-1131)

have reported that B7.1 is superior to B7.2 in the activation of T-cells. The use of B7.1 in solution (as a fusion with antibody constant domains) is reported to provide only modest co-stimulation to T-cells receiving TCR stimulation via an independent source (Linsley P.S. *et al* J.Exp.Med., 1991, 173, 721-730).

There is a need for further and improved anti-CEA antibodies useful in cancer diagnosis and therapy.

The present invention is based on the discovery of a novel anti-CEA antibody termed 806.077 antibody herein.

According to one aspect of the present invention there is provided an anti-CEA antibody comprising complementarity determining regions (CDRs) in which the CDRs have the following sequences:

a) heavy chain

CDR1 DNYMH (SEQ ID NO: 29)

CDR2 WIDPENGDTE YAPKFRG (SEQ ID NO: 31)

CDR3 LIYAGYLAMD Y(SEQ ID NO: 32);

b) light chain

CDR1 SASSSVTYMH (SEQ ID NO: 26)

CDR2 STSNLAS (SEQ ID NO: 27)

CDR3 QQRSTYPLT (SEQ ID NO: 28).

The CDRs or complementarity determining regions are those sequences within the hypervariable loops of antibody variable domains which are believed to be critical in determining the specificity of the antigen-antibody interaction (Kabat, E.A., Lu, T.T., Reid-Miller, M., Perry, H.M. & Gottesman, K.S. (1987). Sequences of Proteins of Immunological Interest. 4th edition. Washington D.C.: United States Dept. of Health and Human Services; the reader is also referred to this reference for details of Kabat antibody residue numbering). CDRs as defined herein however include framework residues where these contribute to binding. For the 806.077 antibody the CDRs were determined by homology with the hypervariable sequences of other murine antibodies. In this specification the terms "VK" and "VH" mean variable regions of the light and heavy antibody chains respectively. Anatomy of the antibody molecule has been reviewed by Padlan (1994) in Molecular Immunology 31, 169-217.

The Light Chain CDRs are:

VK CDR1 Kabat residues 24-34 inclusive, SASSSVTYMH (SEQ ID NO: 26);

VK CDR2 Kabat residues 50-56 inclusive, STSNLAS (SEQ ID NO: 27);

VK CDR3 Kabat residues 89-97 inclusive, QQRSTYPLT (SEQ ID NO: 28);

The Heavy Chain CDRs are:

VH CDR1 Kabat residues 31-35B inclusive, DNYMH (SEQ ID NO: 29);

preferred VH CDR1 Kabat residues are no. 27-35B inclusive, FNIKDNYMH (SEQ ID NO: 30);

VH CDR2 Kabat residues 50-65 inclusive, WIDPENGDTE YAPKFRG (SEQ ID NO: 31)

VH CDR3 Kabat residues 95-102 inclusive, LIYAGYLAMD Y (SEQ ID NO: 32); and

preferred VH CDR3 Kabat residues are no. 93-102 inclusive, HVLIYAGYLA MDY (SEQ ID NO: 33).

Preferably binding affinity for CEA antigen is at least 10E-5M, more preferably binding affinity for CEA is at least 10E-6M, more preferably binding affinity for CEA is at least 10E-7M, more preferably binding affinity for CEA is at least 10E-8M, more preferably binding affinity for CEA is at least 10E-9M, more preferably binding affinity for CEA is at least 10E-10M and especially binding affinity for CEA is at least 10E-11M.

The term antibody as used herein generally means an immunoglobulin molecule (or fragment thereof or modified antibody construct such as scFv which retains specific CEA antigen binding). The CDRs are principally responsible for antigen binding, the non-CDR protein sequence is normally derived from an immunoglobulin but may be derived from immunoglobulin domain of a immunoglobulin super family member.

According to another aspect of the present invention there is provided a CEA antibody comprising the following, optionally humanised, structure:

a heavy chain variable region sequence (SEQ ID NO: 11)

```
EVQLQQSGAE LVRSGASVKL SCTASGFNIK DNYMHWVKQR  40
PEQGLEWIAW IDPENGDTEY APKFRGKATL TADSSSNTAY  80
LHLSSLTSED TAVYYCHVLI YAGYLAMDYW GQGTSVAVSS  120
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and;

a light chain variable region sequence (SEQ ID NO: 9):

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DIELTQSPAI MSASPGEKVT ITCSASSSVT YMHWFQQKPG  40
TSPKLWIYST SNLASGVPAR FSGSGSGTSY SLTISRMEAE  80
DAATYYCQQR STYPLTFGAG TKLELKRA  108;
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or any one of the following constructs thereof:

$F(ab')_2$; F(ab'), Fab, Fv, single chain Fv & V-min.

$F(ab')_2$ fragment constructs are preferred. Any suitable antibody fragment which retains 806.077 antibody binding characteristics is contemplated. For example a recently described antibody fragment is "L-$F(ab)_2$" as described by Zapata (1995) in Protein Engineering, 8, 1057-1062. Disulphide bonded Fvs are also contemplated. Optionally the antibody forms part of a conjugate as described below.

A preferred humanised antibody comprises at least one of the following sequences:

a heavy chain variable region sequence which is VH1 (SEQ ID NO: 55);

a light chain variable region sequence which is VK4 (SEQ ID NO: 71);

a human CH1 heavy chain IgG3 constant region;

a human kappa light chain CL region; and

a human IgG3 hinge region;

optionally in the form of a $F(ab')_2$ fragment.

According to another aspect of the present invention there is provided a polynucleotide sequence capable of encoding for the heavy or light chain variable region of a CEA antibody of the invention. Preferably the heavy or light chain variable region is fused (optionally via some linking sequence) to a gene encoding a protein effector moiety (as part of a conjugate, see text below), preferably fusion is through the antibody heavy chain. Generally fusion can be either at the N or C terminus of the antibody chain. For B7 conjugates fusion at the N-terminus of the antibody chain is preferred.

CPB has an N-terminal pro domain which is believed to assist correct folding of protein before the pro domain is removed to release active enzyme. If proCPB is fused at its C terminus to the N terminus of an antibody chain this allows removal of pro domain (e.g. by trypsin treatment) from the N terminus of the fusion construct. Alternatively if proCPB was attached to the C terminus of an antibody chain then the problem arises of having to remove the pro domain from the "middle" of the construct without destroying the fusion protein. The solution is to co-express the pro domain separately (in trans). This has the advantage, once the cell lines have been constructed, of not requiring trypsin activation of expressed fusion protein to remove CPB pro domain. Constructs with proCPB fused at its C terminus to the N terminus of an antibody chain have the advantage of not requiring

construction of co-expression cell lines which require high level expression of the pro domain along with high level expression of other proteins..

In this specification conservative amino acid analogues of specific amino acid sequences are contemplated which retain the binding properties of the CEA antibody of the invention but differ in sequence by one or more conservative amino acid substitutions, deletions or additions. However the specifically listed amino acid sequences are preferred. Typical conservative amino acid substitutions are tabulated below.

Conservative Substitutions

Original	**Exemplary Substitutions**	**Preferred Substitutions**
Ala (A)	Val; Leu; Ile	Val
Arg (R)	Lys; Gln; Asn	Lys
Asn (N)	Gln; His; Lys; Arg	Gln
Asp (D)	Glu	Glu
Cys (C)	Ser	Ser
Gln (Q)	Asn	Asn
Glu (E)	Asp	Asp
Gly (G)	Pro	Pro
His (H)	Asn; Gln; Lys; Arg	Arg
Ile (I)	Leu; Val; Met; Ala; Phe; Norleucine	Leu
Leu (L)	Norleucine; Ile; Val; Met; Ala; Phe	Ile
Lys (K)	Arg; Gln; Asn	Arg
Met (M)	Leu; Phe; Ile	Leu
Phe (F)	Leu; Val; Ile; Ala	Leu
Pro (P)	Gly	Gly
Ser (S)	Thr	Thr
Thr (T)	Ser	Ser
Tyr (Y)	Trp; Phe; Thr; Ser	Phe
Val (V)	Ile; Leu; Met; Phe; Ala; Norleucine	Leu

In this specification nucleic acid variations (deletions, substitutions and additions) of specific nucleic acid sequences are contemplated which retain which the ability to hybridise under stringent conditions to the specific sequence in question. A hybridisation test is set out in Example 9 hereinafter. However specifically listed nucleic acid sequences are preferred. It is contemplated that peptide nucleic acid may be an acceptable equivalent of polynucleotide sequences, at least for purposes that do not require translation into protein (Wittung (1994) Nature 368, 561).

According to another aspect of the present invention there is provided an antibody or antibody fragment as herein described characterised in that it is humanised.

A humanised antibody, related fragment or antibody binding structure is a polypeptide composed largely of a structural framework of human derived immunoglobulin sequences supporting non human derived amino acid sequences in and around the antigen binding site (complementarity determining regions or CDRs; this technique is known as CDR grafting which often involves some framework changes too, see the Examples below). Appropriate methodology has been described for example in detail in WO 91/09967, EP 0328404 and Queen et al. Proc Natl Acad Sci 86,10029, Mountain and Adair (1989) Biotechnology and Genetic Engineering Reviews 10, 1 (1992) although alternative methods of humanisation are also contemplated such as antibody veneering of surface residues (EP 519596, Merck/NIH, Padlan et al). Preferred humanised 806.077 antibodies are any one of Examples 11-47 or 107-122. A preferred humanised heavy chain variable region is VH1 (see Examples). A preferred light chain variable region is VK4 optionally incorporating any of the additional changes described in Examples 107-109. A preferred human heavy chain constant region is IgG3.

Chimaeric humanised antibodies represent another aspect of the invention. Preparation of chimaeric humanised antibody fragments of antibody 806.077 antibody is described in Example 8 herein. Chimaeric antibodies are generally constructed by combining the variable region from one species with a constant region from another antibody from a different species.

The term "humanised" in relation to antibodies as used herein includes any method of humanisation such as for example CDR grafting or chimaeric antibody preparation or any hybrid thereof such as for example a CDR grafted heavy chain in combination with a chimaerised light chain (see Example 110 for a suitable embodiment).

In particular, a rodent antibody on repeated in vivo administration in man either alone or as a conjugate will bring about an immune response in the recipient against the rodent antibody; the so-called HAMA response (Human Anti Mouse Antibody). The HAMA response may limit the effectiveness of the pharmaceutical if repeated dosing is required. The immunogenicity of the antibody may be reduced by chemical modification of the antibody with a hydrophilic polymer such as polyethylene glycol or by using the methods of genetic engineering to make the antibody binding structure more human like. For example, the gene sequences for the variable domains of the rodent antibody which bind CEA can be substituted for the variable domains of a human myeloma protein, thus producing a recombinant chimaeric antibody. These procedures are detailed in EP 194276, EP 0120694, EP 0125023, EP 0171496, EP 0173494 and WO 86/01533. Alternatively the gene sequences of the CDRs of the CEA binding rodent antibody may be isolated or synthesized and substituted for the corresponding sequence regions of a homologous human antibody gene, producing a human antibody with the specificity of the original rodent antibody. These procedures are described in EP 023940, WO 90/07861 and WO91/09967. Alternatively a large number of the surface residues of the variable domain of the rodent antibody may be changed to those residues normally found on a homologous human antibody, producing a rodent antibody which has a surface 'veneer' of residues and which will therefore be recognized as self by the human body. This approach has been demonstrated by Padlan et.al. (1991) Mol. Immunol. 28, 489.

According to another aspect of the present invention there is provided a host cell transformed with a polynucleotide sequence or a transgenic non-human animal or transgenic plant developed from the host cell in which the polynucloetide sequence encodes at least the variable region of the heavy chain or light chain of a CEA antibody of the invention, optionally in the form of a conjugate as described herein.

According to another aspect of the present invention there is provided hybridoma 806.077 deposited as ECACC deposit no. 96022936 and variant cell lines thereof.

Hybridoma 806.077 antibody was deposited at the European Collection of Animal Cell Cultures (ECACC), PHLS Centre for Applied Microbiology & Research, Porton Down, Salisbury, Wiltshire SP4 0JG, United Kingdom on 29th February 1996 under accession no. 96022936 in accordance with the Budapest Treaty.

According to another aspect of the present invention there is provided plasmid pNG3-Vkss-HuCk deposited as NCIMB deposit no.40798.

Plasmid pNG3-Vkss-HuCk was deposited at The National Collections of Industrial and Marine Bacteria (NCIMB), 23 St Machar Drive, Aberdeen AB2 1RY, Scotland, United Kingdom on 11-April-1996 under deposit reference number NCIMB 40798 in accordance with the Budapest Treaty.

According to another aspect of the present invention there is provided plasmid pNG4-VHss-HuIgG2CH1' deposited as NCIMB deposit no. 40797.

Plasmid pNG4-VHss-HuIgG2CH1' was deposited at The National Collections of Industrial and Marine Bacteria (NCIMB), 23 St Machar Drive, Aberdeen AB2 1RY, Scotland, United Kingdom on 11-April-1996 under deposit reference number NCIMB 40797 in accordance with the Budapest Treaty.

According to another aspect of the present invention there is provided plasmid pNG3-Vkss-HuCk-NEO deposited as NCIMB deposit no. 40799.

Plasmid pNG3-Vkss-HuCk-NEO was deposited at The National Collections of Industrial and Marine Bacteria (NCIMB), 23 St Machar Drive, Aberdeen AB2 1RY, Scotland, United Kingdom on 11-April-1996 under deposit reference number NCIMB 40799 in accordance with the Budapest Treaty.

According to another aspect of the present invention there is provided a method of making at least a variable region of a heavy or light chain of an anti-CEA antibody as herein defined comprising:

a) transforming a host cell with a polynucleotide sequence which encodes at least the variable region of the heavy or light chain of the anti-CEA antibody and optionally developing the transformed host cell into a transgenic non-human mammal or transgenic plant;

b) subjecting the host cell, transgenic non-human mammal or transgenic plant to conditions conducive to expression, and optionally secretion, of at least the variable region and optionally;

c) at least partially purifying the variable region.

According to another aspect of the present invention there is provided a method of making an antibody or a conjugate as defined herein which comprises:

a) subjecting a host cell, a transgenic non-human mammal or a transgenic plant as defined herein, or the 806.077 hybridoma, to conditions conducive to expression, and optionally secretion, of the antibody or conjugate; and optionally

b) at least partially purifying the antibody or conjugate.

Preferably both heavy and light chain variable regions are expressed in the same cell and assembled thereby to form an anti-CEA antibody. Preferably the heavy or light chain variable region is fused (optionally via some linking sequence) to a gene encoding a protein effector moiety (as part of a conjugate, see text below), preferably fusion is through the antibody heavy chain. Generally fusion can be either at the N or C terminus of the antibody chain. For B7 conjugates fusion at the N-terminus of the antibody chain is preferred. CPB has an N-terminal pro domain which is believed to assist correct folding of protein before the pro domain is removed to release active enzyme. If proCPB is fused at its C terminus to the N terminus of an antibody chain this allows removal of pro domain (e.g. by trypsin treatment) from the N terminus of the fusion construct. Alternatively if proCPB was attached to the C terminus of an antibody chain then the problem arises of having to remove the pro domain from the "middle" of the construct without destroying the fusion protein. The solution is to co-express the pro domain separately (in trans). This has the advantage, once the cell lines have been constructed, of not requiring trypsin activation of expressed fusion protein to remove CPB pro domain. Constructs with proCPB fused at its C terminus to the N terminus of an antibody chain have the advantage of not requiring construction of co-expression cell lines which require high level expression of the pro domain along with high level expression of other proteins..

According to another aspect of the present invention there is provided a method of making monoclonal antibody 806.077 comprising:

a) culturing hybridoma 806.077 antibody deposited as ECACC deposit no. 96022936 in medium under conditions conducive to expression of antibody therefrom and;

b) obtaining antibody 806.077 antibody from the culture medium and optionally;

c) preparing a $F(ab')_2$ fragment of antibody 806.077 antibody by enzymic digestion.

According to another aspect of the present invention there is provided a conjugate which comprises an effector moiety and an anti-CEA 806.077 antibody of the invention as herein described. An effector moiety is an entity having the effect of bestowing another activity (e.g. an enzyme, toxin or radioactive ligand) to the 806.077 antibody in forming the conjugate.

In one embodiment, preferably the effector moiety is an enzyme suitable for use in an ADEPT system. In International Patent Application WO 96/20011, published 4-Jul-96, we

proposed a "reversed polarity" ADEPT system based on mutant human enzymes having the advantage of low immunogenicity compared with for example bacterial enzymes. A particular host enzyme was human pancreatic CPB (see for example, Example 15 [D253K]human CPB & 16 [D253R]human CPB therein) and prodrugs therefor (see Examples 18 & 19 therein). The host enzyme is mutated to give a change in mode of interaction between enzyme and prodrug in terms of recognition of substrate compared with the native host enzyme. In our subsequent International Patent Application No PCT/GB96/01975 (published 6-Mar-97 as WO 97/07796) further work on mutant CPB enzyme/ prodrug combinations for ADEPT are described. Preferred enzymes suitable for ADEPT are any one of CPG2 or a reversed polarity CPB enzyme, for example any one of [D253K]HCPB, [G251T,D253K]HCPB or [A248S,G251T,D253K]HCPB.

806.077 Antibody conjugates also have application in tumour immunotherapy. Accordingly in another preferred embodiment the conjugate effector moiety is a co-stimulatory molecule, preferably the co-stimulatory molecule is B7, more preferably human B7.1 or B7.2 and especially human B7.1. Preferably the conjugate is in the form of a fusion protein, preferably in which the fusion protein is formed through linking a C-terminus of the co-stimulatory molecule to an N-terminus 806.077 antibody chain, preferably via the antibody chain heavy chain, preferably in which the 806.077 antibody lacks an Fc antibody region, more preferably a $F(ab')_2$ antibody fragment, more preferably the antibody is humanised or human. An especially preferred conjugate is described in Example 104 below.

The use of antibody to target a co-stimulatory molecule to tumour cells is predicted to bestow the function of antigen presenting to the tumour cells such that T-cells receive specific TCR stimulation from the tumour cell itself and a co-stimulatory signal from the antibody targeted molecule. The use of human or humanised antibodies is preferred for the treatment of human tumours because murine antibodies may evoke an immune reaction when used in man which might result in a reduction in effectivness on repeat therapy. The use of a fusion protein combining a tumour antigen binding region linked to the extracellular portion of a co-stimulatory molecule is novel. Hayden et al (Tissue Antigens, 1996, 48, 242-254) have reported the use of a bi-specific antibody molecule combining an anti-tumour antigen binding domain with an anti-CD28 binding domain. Whilst this molecule is capable of interacting with CD28 on T-cells, the signal it may deliver has the disadvantage of being qualitatively different from that provided by the natural CD28 ligands, for example the affinity of binding

is greater than that between B7.1 and CD28. The cross-species homology between B7.1,B7.2 and CD28,CTLA-4 indicates evolutionary conservation of binding region sequences. Consequently it is believed that, for example B7.1 from man can interact with CD28 from mouse and may impart a similar co-stimulatory signal. For treatment of human disease a human or humanised protein is preferable. However, the use of a human or humanised protein in animal models could produce similar effects to that anticipated in man and such animal models should provide relevant data as to the efficacy of a human/humanised antibody fusion protein with human B7.1/B7.2 in the treatment of human disease.

Conjugation of the effector moiety and antibody may be by any suitable method such as for example chemical linkage via heterobifunctional linkers or recombinant gene fusion techniques. In general fusion proteins are preferred conjugates, particularly for conjugates with HCPB or B7.

Preferred conjugates are those in which the effector moiety is selected from any one of the following:

a) an enzyme suitable for use in an ADEPT system;

b) CPG2;

c) [G251T,D253K]HCPB;

d) [A248S,G251T,D253K]HCPB;

e) a co-stimulatory molecule;

f) extracellular domain of B7;

g) extracellular domain of human B7.1; and

h) extracellular domain of human B7.2;

optionally in the form of a fusion protein.

It will be appreciated that the conjugate of the present invention does not necessarily consist of one effector molecule and one antibody molecule. For example the conjugate may comprise more than one effector molecule per antibody molecule. In general, $F(ab')_2$ antibody conjugates which are fusions between the antibody and an enzyme or an extracellular domain of B7 will have 2 moles of enzyme or B7 per mole of antibody.

Especially preferred conjugates are a fusion protein selected from any one of the following conjugates, (sequences being listed in N terminus to C terminus direction):

a) a humanised 806.077 $F(ab')_2$ - $\{[A248S,G251T,D253K]HCPB\}_2$ fusion comprising:

an antibody Fd' chain of structure VH1(SEQ ID NO: 55)/CH1 constant region from IgG3/hinge region from IgG3;

the Fd' chain being fused via its C terminus to the N terminus of [A248S,G251T,D253K]HCPB; and

an antibody light chain of formula VK4(SEQ ID NO: 71)/CL region from kappa light chain;

b) {[A248S,G251T,D253K]HCPB}$_2$-humanised 806.077 F(ab')$_2$ fusion comprising: [A248S,G251T,D253K]HCPB;

the HCPB being fused at its C terminus, via a $(GGGS)_3$ linker, to the N terminus of an antibody Fd' chain of structure VH1(SEQ ID NO: 55)/CH1 constant region from IgG3/hinge region from IgG3; and

an antibody light chain of formula VK4(SEQ ID NO: 71)/CL region from kappa light chain; and

c) a (human B7.1 extracellular domain)$_2$ - humanised 806.077 F(ab')$_2$ fusion comprising: human B7.1 extracellular domain;

the B7.1 being fused at its C terminus to the N terminus of an antibody Fd' chain of structure VH1(SEQ ID NO: 55)/CH1 constant region from IgG3/hinge region from IgG3; and an antibody light chain of structure VK4(SEQ ID NO: 71)/CL region from kappa light chain.

In this specification the antibody hinge region in relation to conjugates is defined according to the principles set out by Padlan (1994) in Molecular Immunology 31, 169-217: see Table 2 therein in particular. In these especially preferred conjugates there are 2 moles of enzyme or B7.1 per mole of F(ab')$_2$. The forward slash ("/") is merely a separator to indicate discrete structural elements joined by peptide bonds that make up parts of the conjugate.

The VH1 and/or VK4 variable region humanised sequences have the advantage of preserving good binding properties with minimal additional changes required to the human framework. The IgG3 hinge region has the advantage of giving good F(ab')$_2$ production levels and homogeneity of product.

In another preferred embodiment relating to the especially preferred conjugates defined above, fusion is effected through the antibody light chain. In yet another preferred embodiment relating to the especially preferred conjugates defined above, the CH1 constant region from IgG3/hinge region from IgG3 structural element may be replaced by the corresponding IgG2 element.

When the effector molecule is a toxin, this toxin moiety generally comprises a component which possesses cytotoxic properties and hence is capable of killing cells following internalisation.

The toxin moiety and the anti-CEA antibody may be coupled directly to one another, or they may be coupled indirectly. The toxin moiety and the anti-CEA antibody are, in general, coupled such that the geometry of the conjugate permits the anti-CEA antibody to bind to its target cell. Advantageously, the toxin moiety and the anti-CEA antibody are coupled such that the conjugate is extracellularly stable, and intracellularly unstable so that the toxin moiety and the anti-CEA antibody remain coupled outside the target cell, but following internalisation, the toxin moiety is released. Thus, advantageously the conjugate has an intracellularly cleavable/extracellularly stable site.

Examples of conjugates in which the toxin moiety is directly coupled to the target cell binding moiety include those in which the toxin moiety and the anti-CEA antibody are coupled by a disulphide bridge formed between a thiol group on the toxin moiety and a thiol group on the anti-CEA antibody. Details of the preparation and properties of immunotoxins and other conjugates are given in European patent application EP 528 527 (publication no.) the contents of which is incorporated herein by reference thereto.

According to another aspect of the present invention there is provided a polynucleotide sequence capable of encoding a polypeptide of an antibody or a conjugate as defined in any preceding claim. The term "capable of encoding" is intended to encompass polynucleotide sequences taking into account degeneracy in the genetic code in that some amino acids are encoded by more than one codon.

According to another aspect of the present invention there is provided a vector comprising a polynucleotide as defined above.

According to another aspect of the present invention there is provided a host cell transformed with a polynucleotide sequence as defined above or a transgenic non-human animal or transgenic plant developed from the host cell.

According to another aspect of the present invention there is provided a pharmaceutical composition comprising a conjugate of the invention described herein in association with a pharmaceutically-acceptable diluent or carrier, optionally in a form suitable for intravenous administration.

According to another aspect of the present invention there is provided a conjugate as described herein for use as a medicament.

According to another aspect of the present invention there is provided use of a conjugate as described herein for preparation of a medicament for treatment of neoplastic disease.

It will be appreciated that the dose and dosage regimen will depend upon the particular effector moiety employed, the population of the target cell and the patient's history. The dose of the conjugate administered will typically be in the range 0.1 to 1mg/kg of patient weight.

The conjugates of the present invention will normally be administered in the form of a pharmaceutical composition. Thus according to the present invention there is also provided a pharmaceutical compostion which comprises a conjugate (as defined herein) in association with a pharmaceutically-acceptable diluent or carrier. An example of such a formulation is given herein in Example 10.

Pharmaceutical compositions of the present invention may be formulated in a variety of dosage forms. Generally, the conjugates of the present invention will be administered parenterally, preferably intravenously. A particular parenteral pharmaceutical composition is one which is formulated in a unit dosage form which is suitable for administration by injection. Thus, particularly suitable compositions comprise a solution, emulsion or suspension of the immunotoxin in association with a pharmaceutically acceptable parenteral carrier or diluent. Suitable carriers or diluents include aqueous vehicles, for example water or saline, and non-aqueous vehicles, for example fixed oils or liposomes. The compositions may include agents which enhance the stability of the conjugate in the composition. For example, the composition may include a buffer. The concentration of the conjugate will vary, but in general, the conjugate will be formulated at concentrations of about 1 to 10 mg/ml.

According to another aspect of the present invention there is provided an expression vector coding for an anti-CEA antibody of the invention as herein defined.

According to another aspect of the present invention there is provided an expression vector encoding at least the variable region of a heavy or light chain of an anti-CEA antibody as herein defined.

According to another aspect of the present invention there is provided a host cell transformed with a vector as herein described which is compatible with expression therein.

According to another aspect of the present invention there is provided a host cell transformed with a polynucleotide sequence as herein defined.

Mammalian cells (CHO, COS, myeloma) have been used as host for the co-expression of antibody H and L chain cDNAs and fragments thereof to produce antibody with the specified binding activity (Bebbington, C., 1991, Methods, vol 2, p136-145, and Adair, J., 1992, Immunological Reviews, vol 130). For expression of constructs leading to direct expression of active CPB, COS or CHO cell expression systems are preferred. The cDNAs can be introduced on plasmids and allowed to integrate into chromosomal DNA especially for CHO cells or allowed to replicate to very high copy number especially in COS cells. The plasmids generally require a selectable marker for maintenance in transfected hosts, an efficient eukaryotic promoter to allow a high level of transcription from the cDNAs, convenient restriction enzyme sites for cloning and polyadenylation and transcription termination signals for message stabilty. Several such vectors have been described in the literature (Bebbington, C. et al, 1992, Bio/Technology, vol 10, p169-175, and Wright, A., 1991, Methods, vol 2, p125-135) and there are commercially available vectors, (such as pRc/CMV ,Invitrogen Corp.) which are suitable.

The expression of a range of antibody fragments in E.coli is well documented (reviewed by Pluckthun, A., Immunological Reviews, 1992, vol 130, p151-188 and Skerra, A., Current Opinion in Immunology, 1993, vol 5, p256-262). Intracellular expression of Fd and L chains has been described (Cabilly, S., 1989, Gene, vol 85, p553-557) but this may require in vitro refolding and re-association of the chains (Buchner, J and Rudolph, R., 1991, Bio/Technology, vol 9, p157-162) to produce binding activity. A more efficient route to obtaining active antibody fragments is through periplasmic secretion (Better, M. et al, 1988, Science, vol 240, p1041-1043). The H and L chain components of the antibody fragment are co-expressed from a single plasmid. Each antibody chain is provided with a bacterial leader peptide which directs it to the E.coli periplasm where the leader is cleaved and the free chains associate to produce soluble and active antibody fragments. This process is believed to mimic the natural process in eukaryotic cells where the expressed antibody chains pass into the lumen of the endoplasmic reticulum prior to association into whole antibodies. This process often results in the presence of binding activity in the culture supernatant.

Some expression systems involve transforming a host cell with a vector; such systems are well known such as for example in E. coli, yeast and mammalian hosts (see Methods in

Enzymology 185, Academic Press 1990). Other systems of expression are also contemplated such as for example transgenic non-human mammals in which the gene of interest, preferably cut out from a vector and preferably in association with a mammary promoter to direct expressed protein into the animal's milk, is introduced into the pronucleus of a mammalian zygote (usually by microinjection into one of the two nuclei (usually the male nucleus) in the pronucleus) and thereafter implanted into a foster mother. A proportion of the animals produced by the foster mother will carry and express the introduced gene which has integrated into a chromosome. Usually the integrated gene is passed on to offspring by conventional breeding thus allowing ready expansion of stock. Preferably the protein of interest is simply harvested from the milk of female transgenic animals. The reader is directed to the following publications: Simons et al. (1988), Bio/Technology 6:179-183; Wright et al. (1991) Bio/Technology 9:830-834; US 4,873,191 and; US 5,322,775. Manipulation of mouse embryos is described in Hogan et al, "Manipulating the Mouse Embryo; A Laboratory Manual", Cold Spring Harbor Laboratory 1986.

Transgenic plant technology is also contemplated such as for example described in the following publications: Swain W.F. (1991) TIBTECH 9: 107-109; Ma J.K.C. et al (1994) Eur. J. Immunology 24: 131-138; Hiatt A. et al (1992) FEBS Letters 307:71-75; Hein M.B. et al (1991) Biotechnology Progress 7: 455-461; Duering K. (1990) Plant Molecular Biology 15: 281-294.

If desired, host genes can be inactivated or modified using standard procedures as outlined briefly below and as described for example in "Gene Targeting; A Practical Approach", IRL Press 1993. The target gene or portion of it is preferably cloned into a vector with a selection marker (such as Neo) inserted into the gene to disrupt its function. The vector is linearised then transformed (usually by electroporation) into embryonic stem (ES) cells (eg derived from a 129/Ola strain of mouse) and thereafter homologous recombination events take place in a proportion of the stem cells. The stem cells containing the gene disruption are expanded and injected into a blastocyst (such as for example from a C57BL/6J mouse) and implanted into a foster mother for development. Chimaeric offspring can be identified by coat colour markers. Chimeras are bred to ascertain the contribution of the ES cells to the germ line by mating to mice with genetic markers which allow a distinction to be made between ES derived and host blastocyst derived gametes. Half of the ES cell derived gametes will carry the gene modification. Offspring are screened (eg by Southern blotting) to identify those with

a gene disruption (about 50% of progeny). These selected offspring will be heterozygous and therefore can be bred with another heterozygote and homozygous offspring selected thereafter (about 25% of progeny). Transgenic animals with a gene knockout can be crossed with transgenic animals produced by known techniques such as microinjection of DNA into pronuclei, sphaeroplast fusion (Jakobovits et al. (1993) Nature 362:255-258) or lipid mediated transfection (Lamb et al. (1993) Nature Genetics 5 22-29) of ES cells to yield transgenic animals with an endogenous gene knockout and foreign gene replacement.

ES cells containing a targeted gene disruption can be further modified by transforming with the target gene sequence containing a specific alteration, which is preferably cloned into a vector and linearised prior to transformation. Following homologous recombination the altered gene is introduced into the genome. These embryonic stem cells can subsequently be used to create transgenics as described above.

The term "host cell" includes any procaryotic or eucaryotic cell suitable for expression technology such as for example bacteria, yeasts, plant cells and non-human mammalian zygotes, oocytes, blastocysts, embryonic stem cells and any other suitable cells for transgenic technology. If the context so permits the term "host cell" also includes a transgenic plant or non-human mammal developed from transformed non-human mammalian zygotes, oocytes, blastocysts, embryonic stem cells, plant cells and any other suitable cells for transgenic technology.

According to another aspect of the present invention there is provided a method of treatment of a human or animal in need of such treatment which comprises administration to a human or animal of a pharmaceutically effective amount of a conjugate as herein described.

According to another aspect of the present invention there is provided a method of targeting an effector moiety to cells displaying antigen CEA in a mammal in need of such targeting which comprises administration of a pharmaceutically effective amount of an conjugate of the invention as herein defined.

According to another aspect of the present invention there is provided the use of an antibody as hereinbefore described in a diagnostic method.

One diagnostic method is immunoassay. An immunoassay for in vitro testing based upon the novel antibody according to the invention may be designed in accordance with conventional immunological techniques in the art, utilising the antibody according to the invention in a labelled or unlabelled form and determining the complex formation of the

antibody with CEA in the sample to be tested. In one case, the antibody may be labelled with a detectable label, such as radiolabel, a chemiluminescer, a fluorescer or an enzyme label. Alternatively the antibody is detected via a complex formed with a labelled substance or by non-labelling techniques, such as biosensor methods eg based upon surface plasmon resonance. The sample may, for example, be in the form of a body fluid, such as serum, or a tissue preparation (histochemical assay).

For in vivo diagnostic purposes, the antibody according to the invention is provided with a suitable externally detectable label, such as eg. a radiolabel or a heavy metal atom, and administered to a subject whereupon the possible localised accumulation of antibody in the body is determined.

For the in vitro diagnosis of cancer the anti-CEA antibody can be conjugated to either enzymes such as horse radish peroxidase and bacterial luciferase which can generate a signal which can be measured or to fluorescent markers or radioisotopes which can be detected and quantitated directly. In a standard immunoassay system such conjugates provide a means of measuring the presence or absence of CEA in body tissues and consequently provides a rapid and convenient test for the diagnosis of tumour disease. See general descriptions of the methodology involved in Enzyme Immunoassay, E.T. Maggio, CRC Press and US 3690 8334, US 3791 932, US 3817 837, US 3850 578, US 3853 987, US 3867 517, US 3901 654, US 3935 074, US 3984 533, US 3996 345 and US 4098 876.

For the in vivo diagnosis of cancer, the anti-CEA antibody can be conjugated to isotopes of elements such as yttrium, technetium or indium or heavy metal isotopes which can be detected by whole body imaging cameras (see Larson, S.M. ,1987, Radiology, 165, 297-304.

For the therapy of cancer, preferred embodiments involve an anti-CEA antibody that can be conjugated to an effector moiety which can kill the cancer cells directly or especially via activation of a suitable prodrug in an ADEPT system. In ADEPT selective killing of tumour cells is achieved by conjugating the anti-CEA antibody to an enzyme which is capable of catalysing the conversion of a non-toxic dose of a prodrug into a potent toxic drug compound. Administration of the conjugate leads to localization of the enzyme activity at the tumour site. Subsequent administration of the prodrug leads to local production of the toxic drug and selective kill at the tumour site. This approach is described in WO 88/07378, US

4,975,278, US 5,405,990 and WO89/10140. Antibody 806.077 may also be used conjugated to a co-stimulatory molecule for tumour immunotherapy as described above.

Selective cell killing of tumour cells can also be achieved by conjugation of the anti-CEA antibody either directly or by chemical derivatization with macrocycle chelators containing high energy radioisotopes such as ^{90}Y, ^{131}I and ^{111}In. The anti-CEA antibody serves to localize the isotope to the tumour and the radiation emitted by the isotope destroys the DNA of the surrounding cells and kills the tumour.

Selective killing of tumour cells can also be achieved by conjugation of the anti-CEA antibody to cytotoxic and cytostatic drugs such as methotrexate, chlorambucil, adriamycin, daunorubicin and vincristine. These drugs have been used in the clinic for many years and the therapy they provide is often limited by non specific toxicity. Conjugation of these drugs to the CEA antibody enables these drugs to localize at the tumour site and thus increasing the dose of drug that can be delivered to the tumour without incurring unacceptable side effects from the action of such drugs on other tissues such as the bone marrow or nervous system.

The effectiveness of the antibody is in many applications improved by reducing the size of the antibody binding structure and thereby improving the tissue penetration and other pharmacodynamic properties of the pharmaceutical composition. This can be achieved by removing the Fc region of the antibody molecule either enzymically or by genetic engineering methods to produce a recombinant Fab' or $F(ab')_2$ fragment.

Genetic engineering methods can also be used to further reduce the size of the anti-CEA antibody. The Fv which contain the CDRs can be engineered and expressed in isolation and chemically cross linked for instance by the use of disulphide bridges. Alternatively, both the light and heavy chain domains making up the Fv structure may be produced as a single polypeptide chain (SCFv) by fusing the Fv domains with a linker peptide sequence from the natural C-terminus of one domain to the N-terminus of the other domain (see PCT/US/87/02208 and US 4704692). Alternatively, a single Fv domain may be expressed in isolation forming a single domain antibody or dAb as described by Ward et al Nature(1989) 341, 544. Another type of anti-CEA antibody contemplated is a V-min construct as disclosed in International Patent Application WO 94/12625 (inventors Slater & Timms).

Abbreviations used herein include:

ADEPT	antibody directed enzyme prodrug therapy
APC	antigen presenting cell
CDRs	complementarity determining regions
CEA	Carcinoma Embryonic Antigen
CL	constant domain of antibody light chain
CPB	carboxypeptidase B
CPG2	carboxypeptidase G2
DAB	substrate 3,3'-diaminobenzidine tetrahydrochloride
DEPC	diethylpyrocarbonate
DMEM	Dulbecco's modified Eagle's medium
ECACC	European Collection of Animal Cell Cultures
EIA	enzyme immunoassay
ELISA	enzyme linked immunosorbent assay
FCS	foetal calf serum
Fd	heavy chain of Fab, Fab' or $F(ab')_2$ optionally containing a hinge
HAMA	Human Anti Mouse Antibody
HCPB	human carboxypeptidase B, preferably pancreatic
hinge (of an IgG)	a short proline rich peptide which contains the cysteines that bridge the 2 heavy chains
HRPO	horse radish peroxidase
NCA	non-specific cross reacting antigen
NCIMB	National Collections of Industrial and Marine Bacteria
PBS	phosphate buffered saline
PCR	polymerase chain reaction
preproCPB	proCPB with an N-terminal leader sequence
proCPB	CPB with its N-terminal pro domain
SDS-PAGE	sodium dodecyl sulphate - polyacrylamide gel electrophoresis

TBS	Tris-buffered Saline
VH	variable region of the heavy antibody chain
VK	variable region of the light antibody chain

The invention is illustrated by the following non-limiting Examples (supported by Reference Examples which follow the Examples) in which:

Figure 1 shows anti-tumour activity of 806.077 antibody-CPG2 conjugate in an ADEPT model;

Figure 2 shows a plasmid map of pCF009;

Figure 3 shows BIAcore data showing antibody-B7.1 fusion protein binding to immobilised CTLA4-Ig in which the solid line represents test binding and the dotted line is a blank control; and unless otherwise stated;

DNA is recovered and purified by use of GENECLEAN™ II kit (Stratech Scientific Ltd. or Bio 101 Inc.). The kit contains: 1) 6M sodium iodide; 2) a concentrated solution of sodium chloride, Tris and EDTA for making a sodium chloride/ethanol/water wash; 3) Glassmilk- a 1.5 ml vial containing 1.25 ml of a suspension of a specially formulated silica matrix in water. This is a technique for DNA purification based on the method of Vogelstein and Gillespie published in Proceedings of the National Academy of Sciences USA (1979) Vol 76, p 615. Briefly, the kit procedure is as follows. To 1 volume of gel slice is added 3 volumes of sodium iodide solution from the kit. The agarose is melted by heating the mix at 55^{o}C for 10 min then Glassmilk (5-10ml) is added, mixed well and left to stand for 10 min at ambient temperature. The glassmilk is spun down and washed 3 times with NEW WASH (0.5ml) from the kit. The wash buffer is removed from the Glassmilk which is to dry in air. The DNA is eluted by incubating the dried Glassmilk with water (5-10ml) at 55^{o}C for 5-10 min. The aqueous supernatant containing the eluted DNA is recovered by centrifugation. The elution step can be repeated and supernatants pooled;

Competent E. coli DH5α cells were obtained from Life Technologies Ltd (MAX efficiency DH5α competent cells);

Mini-preparations of double stranded plasmid DNA were made using the RPM™ DNA preparation kit from Bio101 Inc. (cat. No 2070-400) or a similar product - the kit contains alkaline lysis solution to liberate plasmid DNA from bacterial cells and glassmilk in

a spinfilter to adsorb liberated DNA which is then eluted with sterile water or 10mM Tris-HCl, 1mM EDTA, pH 7.5;

Serum free medium is OPTIMEM™ I Reduced Serum Medium, GibcoBRL Cat. No. 31985;

LIPOFECTIN™ Reagent (GibcoBRL Cat. No. 18292-011) is a 1:1 (w/w) liposome formulation of the cationic lipid N-[1-(2,3-dioleyloxy)propyl]-n,n,n-trimethylammonium chloride (DOTMA) and dioleoyl phosphatidylethanolamine (DOPE) in membrane filtered water. It binds spontaneously with DNA to form a lipid-DNA complex - see Felgner et al. in Proc. Natl. Acad. Sci. USA (1987) 84, 7431;

G418 (sulphate) is GENETICIN™, GibcoBRL Cat. No 11811, an aminoglycoside antibiotic related to gentamicin used as a selecting agent in molecular genetic experiments;

AMPLITAQ™ ,available from Perkin-Elmer Cetus, is used as the source of thermostable DNA polymerase; and

General molecular biology procedures can be followed from any of the methods described in "Molecular Cloning - A Laboratory Manual" Second Edition, Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory, 1989).

Example 1

Discovery and establishment of hybridoma cell line 806.077

BALB/C mice, 8 to 10 weeks old, were immunised subcutaneously with a primary dose of CEA (10μg) in phosphate buffered saline solution (0.1ml) and Freund's Complete adjuvant (0.1ml). Two weeks later and again 2 weeks later the animals were boosted with further doses of CEA (10μg) in phosphate buffered saline (0.1ml) mixed with Freund's Incomplete adjuvant (0.1ml). Thirty two weeks later the animals were given a final intravenous immunisation of CEA (10μg) in phosphate buffered saline and sacrificed three days later. The spleens were removed and prepared and fused with NS0 cells (available from the European Collection of Animal Cell Cultures under the accession No. 85110503) by standard methods (Kohler and Milstein, Nature (1975) 256, 495). The resulting cells were distributed into 96-well culture dishes and incubated for 2 weeks. The supernatants from the resulting hybridomas were screened by EIA (enzyme immunoassay). From a total of 1,824 wells generated from 5 fusions, 102 wells were positive against native CEA. In fusion 806, seventeen wells were found to be positive. The cells contained in these wells were cloned by

limiting dilution, and the resulting clones tested by EIA. Lines from 10/17 original wells cloned successfully. One line, designated 806.077, has been deposited with the European Collection of Animal Cell Cultures under Accession No. 96022936. The table below provides a summary of the antibody generation programme that led to discovery of the 806.077 antibody hybridoma.

Antigen	**housing**	**rest weeks**	**number fusions**	**number Wells tested**	**number CEA* +ve by EIA**	**number finally selected**
Untreated CEA	normal	8-20	28	13,920	99	0
desialated CEA	normal	8-12	14	5,568	12*	0
conjugated CEA	normal	10-12	8	3,168	1	0
Untreated CEA	isolator	>30	5	1,824	102	3

* tested against untreated CEA. desialated immunisations produced lots of +ves when tested against the immunogen

Example 2

Preparation of 806.077 antibody from deposited hybridoma cell line ECACC No. 96022936

2.1 Preparation from serum containing medium

A 1ml cryopreserved ampoule was removed from storage in liquid nitrogen and rapidly thawed in a 37°C water bath. The contents were aseptically transferred to a sterile 15ml centrifuge tube. The cells were resuspended by dropwise addition of 10ml of Dulbecco's modified Eagle's medium (DMEM) containing 10% (v/v) foetal calf serum (FCS) accompanied by gentle mixing. The suspension was centrifuged at 50 x g for 10 min, the

supernatant aseptically removed and the pellet resuspended in 5ml of DMEM, 10% FCS and 1% L-glutamine in a 95% air 5% carbon dioxide pre-gassed 25ml tissue culture flask. The flask was incubated at 36.5°C in the dark.

After 3 days the flask was sub-cultured by passing the contents of the entire flask into a larger 75ml flask diluting with DMEM, 10% FCS and 1% L-glutamine (final viable density = 2-3x10^5 cells/ml). Further expansion to 162ml flasks was performed in a similar manner.

Culture supernatants for purification were prepared in 500ml roller cultures in 850ml roller bottles. Cultures were seeded at 2x10^5 viable cells/ml in pre-gassed roller bottles, rotated at 3rpm and incubated at 36.5°C. Cultures were grown to maturity and harvested typically 500-800 hours after inoculation when the cell viability was below 10% and IgG concentration had reached a maximum.

2.2 Treatment of culture harvests

After harvest, roller bottle culture supernatants were clarified by centrifugation at 60 x g for 30 minutes. Sodium azide (0.02% w/v) was added as a preservative to the clarified supernatant which was stored at 4°C in the dark until purification.

2.3 Purification of 806.077 antibody

806.077 Antibody hybridoma supernatant (3l) was adjusted to pH 7.5 with dilute aqueous sodium hydroxide and filtered through a 0.45µm filter (Millipore MILLIDISK™). The filtered antibody supernatant was loaded onto an affinity column of Protein G (for example Protein G Fast Flow SEPHAROSE™, Pharmacia product code 17.0618.03; 5cm i.d x 6.5cm = 130ml;) equilibrated in phosphate buffered saline ("PBS"; 8mM Na_2HPO_4, 1.5mM KH_2PO_4, 150mM NaCl, 2.5mM KCl, pH 7.3, for example as available in tablet form for reconstitution from Oxoid) at 4°C at a flow-rate of 4ml/min. The column was washed with PBS (260ml) at the same flow rate and the antibody eluted with 100mM sodium citrate pH 2.6, collecting fractions and monitoring the eluate by UV absorption (280nm). The UV absorbing fractions containing the antibody, were bulked, immediately adjusted to pH 7 and concentrated to about 2mg/ml by ultrafiltration using a 30 kDa cut-off membrane (e.g. Amicon YM30). Dialysis, using a 6-8 kDa porosity cut-off membrane (e.g. SPECTRAPOR™ 1) membrane, into 50mM tris-HCl pH 7.0 buffer yielded 110mg 806.077 antibody, >95% pure by SDS-PAGE.

Example 3

Selectivity f 806.077 antibody

To assess selectivity, many human normal and tumour tissues have been screened for reactivity with the antibody 806.077, using sensitive three-stage indirect immunohistology on acetone-fixed, frozen cryostat sections.

Immunohistology was carried out on sections of human tissue obtained either at resection surgery or at post mortem. To preserve optimal morphology and antigenicity, tissues were obtained as fresh as possible, cut into small pieces (about $0.5cm^3$) and flash frozen in liquid nitrogen prior to storage at -80°C. Sections of tissue (6μ) were cut on a cryostat, mounted on polylysine coated slides (e.g. blue TECHMATE™ slides, Dako) and fixed in ice-cold acetone for 2 minutes before being wrapped in foil and stored at -80°C.

Slides were allowed to defrost at room temperature before being unwrapped from the foil immediately prior to use. Each section was outlined with a diamond marker, and to each section was added either 100μl 806.077 antibody diluted to 2 μg/ml in Tris-buffered Saline (TBS), or 100μl CEA/NCA reactive control (A5B7 antibody) at 2μg/ml in TBS, or 100μl MOPC isotype control (Sigma Chemical Company, St. Louis, U.S.A., Cat. No. M 9269) at 2μ g/ml in TBS, or relevant positive control such as LP34 (Dako). All subsequent incubations were carried out at room temperature for 30 minutes in a humidified chamber: all wash steps were in TBS with 2 changes. After incubation, the slides were washed and 100μl of second antibody reagent, comprising 1/50 rabbit anti-mouse immunoglobulins conjugated to horse radish peroxidase (Dako Patts) and 1/5 normal human serum (Sigma) in TBS was added to each section.

The slides were again incubated and washed in TBS. A final detecting antibody, 100 μl swine anti-rabbit immunoglobulin conjugated to horse radish peroxidase (1/50 dilution with 1/5 normal human serum in TBS), was added to each section, incubated and washed thoroughly. DAB substrate (3,3'-diaminobenzidine tetrahydrochloride) was prepared using 1 DAB tablet (Sigma) with hydrogen peroxide (17μl) in TBS (17ml), and added dropwise through a fast filter paper (e.g. Whatman Number 4). After 3 minutes incubation the excess DAB was tapped off the slides and the slides were washed in TBS. After counter staining with haematoxylin (e.g. Mayer's Haematoxylin, Shandon) sections were dehydrated in alcohol and xylene, and mounted in non-aqueous synthetic mountant (e.g. E-Z mountant, Shandon) before examination under a microscope.

The areas of antibody bonding were visualised by brown staining on the section. A scoring system was used to evaluate the degree of binding of 806.077 antibody to tissues:

+++ (strong)	= antibody binding to >75% tumour cells
++ (moderate)	= antibody binding to 50%- 75% tumour cells
+ (weak)	= antibody binding to 25% - 50% tumour cells
+/- (minimal)	= non-focal antibody binding to a small area of tumour cells
-	= no staining

Carcinoembryonic antigen (CEA) is a member of the immunoglobulin gene superfamily with one predicted variable-like domain region (N domain; 108 amino acids) and three sets of constant domain-like regions A1B1, A2B2 and A3B3; 92 amino acids for A domains and 86 amino acids for B domains (Hefta, 1992, Cancer Research 52:5647-5655. In addition, CEA possesses two signal peptides, one at the amino terminus and one at the carboxyl terminus. Both are removed during post-translational processing, the one at the carboxy terminus being replaced by a glycosylphosphatidylinositol (GPI) moiety.

A large number of CEA-related proteins with varying homology to CEA have been reported (Thompson, 1991, J. of Clinical Laboratory Analysis, 5: 344-366). These include non-specific cross reacting antigens, NCA 1 and 2. These related proteins are expressed on a range of normal tissues including granulocytes and normal lung epithelium. The majority of anti-CEA monoclonal antibodies generated so far, cross react with one of these related proteins and thus react with a range of normal tissues and often react strongly with either granulocytes or lung epithelium.

Anti-CEA antibody, 806.077 was identified as being CEA selective, exhibiting no cross reactivity to granulocytes and only minimal staining to 4/14 normal lung tissues tested.

806.077 antibody was initially screened for tumour and NCA selectivity as a tissue culture supernatant. The screens were carried out using the supernatant neat and diluted at 1:10 and demonstrated equivalent binding of the antibody to colon tumours when compared to A5B7, but much reduced binding to normal lung and spleen tissues when compared to the same antibody. The antibody was affinity purified (as described in Example 2) and the screens repeated and extended to include further tumours and tissue types.

The antibody was titrated against a panel of colo-rectal tumour sections and this screen demonstrated the optimum screening concentration of 806.077 antibody to be 2μg/ml. All subsequent screens were carried out using the antibody at this concentration.

The results of these screens were as follows. The reactivity of 806.077 antibody was compared against A5B7 (also screened at 2μg/ml) against the following tumours/normal tissues:

806.077 antibody Tumour reactivity:

Colon tumours (n = 17).

Moderate to strong reactivity (++/+++ equivalent to A5B7) was seen to all 17 tumours tested .

Breast tumours (n=6).

Moderate/weak staining (+/++), 2/6 tumours; minimal staining(+/-), 2/6 tumours.

NSCLC tumours (n=6).

Strong staining (+++), 2/6 tumours; moderate staining (++), 1/6 and weak staining (+), 2/6 tumours.

Gastric tumours (n=2).

Strong staining (+++), 1/2 tumours; weak staining (+) 1/2 tumours.

Ovary tumours (n=3) and prostate tumours (n=3).

No staining was seen to any of these tumours.

In all cases, equivalent reactivity was seen with A5B7.

Normal tissue reactivity:-

Lung (NCA reactivity) (n=14).

Weak staining (+), 4/14 lung tissues; no staining (-) 10/14 tissues.

A5B7 bound moderately (++), 1/14 lung tissues; weakly (+), 10/14 tissues and minimally (+/-), 1/14 tissues.

Spleen (granulocyte/NCA reactivity) (n=6).

No staining was seen to any of the spleen tissues tested.

A5B7 bound moderately (++), 1/6 tissues and weakly (+), 5/6 tissues

Post mortem normal tissues (n=13).

Moderate/weak reactivity (++/+) was seen only to oesophagus, skin, colon and pancreas tissues (CEA expressing normal tissues). Similar binding was seen with A5B7. In addition to the positive tissues, colon, skin, oesophagus and pancreas, the negative tissues were: cerebellum, mid-brain, cerebrum, smooth muscle, liver, kidney, aorta, stomach, heart.

Example 4

Generation f 806.077 antib dy F(ab') fragment

Ficin (10mg) was suspended in a solution of 50mM cysteine (3ml; BDH 37218) and 50mM tris-HCl pH 7.0 and incubated at 37°C for 30minutes. Excess cysteine was removed by size exclusion chromatography (Sephadex™ G-25 column, 1.5cmx25cm; Pharmacia) in 50mM tris-HCl pH 7.0 buffer. The reduced ficin concentration was determined by monitoring UV absorbance at A280nm (assuming that a 1mg/ml solution has an absorbance reading of 2 in a 1cm cell) and was found to be 1.65mg/ml.

A solution of 806.077 antibody (100mg) in 50mM tris-HCl buffer pH 7.0 (50ml) and freshly reduced ficin (5mg; 3ml of the above solution) was digested at 37°C over 20 hours. The digest was then diluted with an equal volume of PBS and loaded onto a Protein G affinity column (Pharmacia SEPHAROSE™ Fast Flow, 5.0cm i.d x 6.5cm = 125ml; previously equilibrated with 50mM tris-HCl pH 7.0 buffer at 4°C), at a constant flow-rate of 3ml/min. The column was washed with 50mM sodium acetate pH 4.0 (250ml) to remove low M.W. fragments, followed by 50mM sodium citrate pH 2.8 to elute the $F(ab')_2$, monitoring the UV adsorbance of the eluate at A280nm. The $F(ab')_2$ containing eluate was adjusted to pH 7 and buffer exchanged into 100mM sodium phosphate/100mM sodium chloride/1mM EDTA pH 7.2 by dialysis and concentrated to 8mg/ml by membrane filtration using a 10 kDa cut-off (e.g. Amicon™ YM10) assuming that a 1mg/ml solution has an absorbance reading at 280nm of 1.4 in a 1cm cell. A 65% yield of 42mg 95% pure $F(ab')_2$ was obtained.

Example 5

Preparation of 806.077 antibody $F(ab')_2$ - carboxypeptidase G2 conjugate

The linker for 806.077 antibody $F(ab')_2$ derivatisation was **SATA** (S-acetyl thioglycollic acid N-hydroxysuccinimide ester, Sigma, product code A 9043)
The linker for carboxypeptidase G2 (CPG2) derivatisation was **SMPB** [4-(p-maleimidophenyl) butyric acid N-hydroxysuccinimide ester, Sigma, product code M6139]

5.1 $F(ab')_2$ derivatisation:

To a solution of the $F(ab')_2$ fragment (40mg, prepared as described in **Example 4**) in 100mM phosphate/100mM NaCl/1mM EDTA pH 7.2 (buffer A; 5ml) was mixed with SATA (0.28mg) in DMSO (28µl). After 40 minutes at room temperature the resulting solution was applied to a desalting column (SEPHADEX™ G-25, 1.5cm i.d x 50cm =100ml; equilibrated

in buffer A at 4°C) at a flow-rate of 1.2ml/min. to remove excess reagents. The eluate was monitored by UV absorption at A280nm. The SATA derivatised $F(ab')_2$ was pooled and mixed with 10% v/v 500mM hydroxylamine HCl/500mM sodium phosphate/30mM EDTA pH 8.0 for 60minutes at room temperature to deacetylate the derivatised $F(ab')_2$. The protein concentration was determined by UV absorption at 280nm assuming that a 1mg/ml solution has an absorbance reading of 1.4 in a 1cm cell. The solution was diluted to about 1mg/ml with buffer A. The linker loading was determined by Ellman's -SH assay and found to be 1.8 -2.0 linkers / mole $F(ab')_2$.

5.2 CPG2 derivatisation:

Large scale purification of CPG2 from Pseudomonas RS-16 was described in Sherwood et al. (1985), Eur, J. Biochem., 148, 447 - 453. Preparation of $F(ab')_2$ and IgG antibodies coupled to CPG enzyme may be effected by known means and has been described for example in PCT WO 89/10140. CPG may be obtained from Centre for Applied Microbiology and Research, Porton Down, Salisbury, Wiltshire SP4 0JG, United Kingdom. CPG2 may also be obtained by recombinant techniques. The nucleotide coding sequence for CPG2 has been published by Minton, N.P. et al., Gene, (1984) 31, 31-38. Expression of the coding sequence has been reported in E.coli (Chambers, S.P. et al., Appl. Microbiol, Biotechnol. (1988), 29, 572-578) and in Saccharomyces cerevisiae (Clarke, L. E. et al., J. Gen Microbiol, (1985) 131, 897-904). Total gene synthesis has been described by M. Edwards in Am. Biotech. Lab (1987), 5, 38-44. Expression of heterologous proteins in E.coli has been reviewed by F.A.O. Marston in DNA Cloning Vol. III, Practical Approach Series, IRL Press (Editor D M Glover), 1987, 59-88. Expression of proteins in yeast has been reviewed in Methods in Enzymology Volume 194, Academic Press 1991, Edited by C. Guthrie and G R Fink.

CPG enzyme is available from Sigma Chemical Company, Fancy Road, Poole, Dorset, U.K. CPG enzyme was described in: Goldman, P. and Levy, C.C., PNAS USA, 58: 1299-1306 (1967) and in: Levy, C.C. and Goldman P., J. Biol. Chem., 242: 2933-2938 (1967). Carboxypeptidase G3 enzyme has been described in Yasuda, N. et al., Biosci. Biotech. Biochem., 56: 1536-1540 (1992). Carboxypeptidase G2 enzyme has been described in European Patent 121 352.

CPG2 (50mg; recombinant enzyme from E. coli) was dialysed into 100mM sodium phosphate/100mM sodium chloride pH 7.2 (=buffer B) and diluted to 8mg/ml, assuming that a 1mg/ml solution has an absorbance reading at 280nm of 0.6 in a 1cm cell.

SMPB(Sigma) was dissolved in DMSO at 10mg/ml. CPG2 (50mg in buffer B at 8mg/ml) was mixed with the SMPB solution (0.108ml; 1.08mg), and reacted at room temperature for 120 minutes. Excess reagents were removed on a desalting column (Sephadex G-25, 1.5cm i.d x 50cm = 100ml; equilibrated in buffer B at 4°C) at 1.2ml/min. Derivatised CPG2 was pooled and the concentration determined by UV A280nm, assuming that a 1mg/ml solution has an absorbance reading at 280nm of 0.6 in a 1cm cell. The solution was diluted to a CPG2 concentration of about 1mg/ml. The linker loading was determined by a 'reverse' Ellman's assay, by adding a known amount of 2-mercaptoethanol to the maleimido-derivatised CPG2 and assaying unreacted -SH. A linker loading of 2.0-2.4 linkers / mole CPG2 was found.

5.3 Conjugation:

Equal weights of the deacetylated derivatised $F(ab')_2$ and derivatised CPG2 were mixed under nitrogen and the mixture (about 80ml, at a total protein concentration of about 1mg/ml) left at room temperature for 20h. The reaction was terminated by the addition of 10% v/v 100mM aqueous glycine. The crude conjugation mixture was buffer exchanged by dialysis into a low salt buffer (50mM sodium acetate pH 6.0) and applied to a dye-ligand affinity column (where the dye binds to CPG2 e.g. ACL Mimetic Green 1, 2.5cm i.d x10cm = 50ml) at 4°C equilibrated in the same buffer, to remove unreacted derivatised $F(ab')_2$. The conjugate and derivatised CPG2 were eluted with 50mM acetate/ 500mM NaCl pH 6.0, at a flow rate of 2.0ml/min monitoring the elution by UV (A280nm).

The crude conjugate, still containing derivatised CPG2, was concentrated using a 10 kDa cut-off ultrafiltration device (e.g. Amicon YM10™) to about 12ml, at 5mg/ml total protein concentration and 10% v/v 10mM zinc sulphate (Sigma Z 0251) in water was added to replenish zinc lost to the CPG2 in the process. Further chromatography by size exclusion (e.g. SEPHACRYL S-300HR™ Pharmacia, 2.5cm i.d x 25cm = 500ml) at 4°C in 50mM sodium acetate / 150mM sodium chloride pH 6.0 at a flow-rate of 1ml/min., collecting fractions and monitoring by UV A280nm, resulted in the fractionation of the conjugate and its separation from unreacted derivatised CPG2, as determined by SDS-PAGE of column fractions.

The peak containing conjugate (with ratios of $F(ab')_2$:CPG2 of 1:2, 1:1 and 2:1) was pooled and concentrated by ultrafiltration to 1.3mg/ml, the protein concentration being determined by monitoring UV adsorbance at A280nm (assuming 1mg/ml has an absorbance of 1.0). Purity of the conjugate was determined by SDS PAGE and found to contain a total of 12mg conjugate with the composition 65% 1:1 ratio conjugate, 20% 1:2 or 2:1 ratio conjugate with < 5% free derivatised $F(ab')_2$ and < 5% free derivatised CPG2.

Example 6

Anti-tumour activity of 806.077 antibody $F(ab')_2$-CPG2 conjugate in combination with a prodrug.

The anti-tumour activity of the 806.077 antibody $F(ab')_2$-CPG2 conjugate prepared as described in Example 5 was evaluated in combination with the prodrug N(4-[N,N-bis(2-chloroethyl)amino]-phenoxycarbonyl)-L-glutamic acid (called "PGP" in this example, is described in Example 1 in US 5,405,990 and Blakey et al., Br. J. Cancer 72, 1083-88, 1995) in a human colorectal tumour xenograft model.

Groups of 8-10 female athymic nude mice were injected s.c. with 1×10^7 LoVo colorectal tumour cells (ECACC no 87060101). When the tumours were 4-5 mm in diameter either 806.077 antibody $F(ab')_2$-CPG2 conjugate (250 U CPG2 enzyme activity Kg^{-1}) or phosphate buffered saline (170 mM NaCl, 3.4 mM KCl, 12 mM Na_2HPO_4, 1.8 mM KH_2PO_4, pH 7.2) was injected intravenously (i.v). Seventy-two hours later PGP prodrug was injected i.p. (3 doses of 40 mg/Kg at 1 h intervals). The length of the tumours in two directions was then measured three times a week and the tumour volume calculated using the formula:

$$\text{Volume} = \Pi/6 \times D^2 \times d$$

where D is the larger diameter and d is the smaller diameter of the tumour. Tumour volume was expressed relative to the tumour volume at the time of initiation of the prodrug arm of the therapy. The anti-tumour activity was compared with control groups given PBS instead of either conjugate or prodrug. Anti-tumour activity was expressed both as a growth delay defined as the time it takes treated tumours to increase their volume by 4-fold minus the time it takes control tumours to increase their volume 4-fold and as a T/C value defined as the volume of the treated tumour divided by the volume of the control tumour 14 days after prodrug administration. Statistical significance of the anti-tumour effects was judged using the analysis of variance (one-way) test.

The anti-tumour activity of 806.077 antibody F(ab')$_2$-CPG2 conjugate in combination with PGP prodrug are shown in Fig 1 and the anti-tumour data is summarised below.

Anti-tumour activity of 806.077 antibody F(ab')$_2$-CPG2 conjugate in combinati n with PGP prodrug in LoVo tumour xenografts.

Conjugate	Dose (U/kg)	T/C (%)	Growth delay (days)	Significance (p)
806.077 F(ab')$_2$-CPG2	250	16.5	14	<0.01
	500	4.7	22	<0.01

The results demonstrate that the 806.077 antibody F(ab')$_2$-CPG2 conjugate in combination with the PGP prodrug produce tumour regressions and prolonged growth delays which were statistically significant compared with control groups.

Example 7

Cloning and sequencing of the variable regions of 806.077 antibody heavy and light chain genes

7.1 Preparation of cytoplasmic RNA

There are several procedures for the isolation of polyA+ mRNA from eukaryotic cells (Sambrook J., Fritsch E.F., Maniatis T., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Second Edition, 1989, Chapter 8, p3 herein referred to as "Maniatis"). In this particular case cytoplasmic RNA was prepared as described by Favoloro et al.., Methods in Enzymology 65, 718-749, from a frozen hybridoma cell pellet containing $1x10^9$ cells which had been stored at -80°C.

The cells were resuspended in 5ml ice-cold lysis buffer (140mM NaCl, 1.5mM $MgCl_2$, 10mM Tris-HCl pH 8.6 and 0.5% NP40 (a polyglycol ether nonionic detergent; Nonylphenoxy Polyethoxy Ethanol, Sigma Cat. No. 127087-87-0)) containing 400u of a ribonuclease inhibitor (RNAguard; Pharmacia Cat. No. 27-0815-01) and vortexed for 10s. This solution was overlayed on an equal volume of ice cold lysis buffer containing 24% (w/v) sucrose and 1% NP-40 and stored on ice for 5 min. The preparation was then centrifuged at 4000 rpm for 30 min at 4°C in a bench top centrifuge (Sorval RT6000B) after which, the

upper cytoplasmic phase was removed to an equal volume of 2 x PK buffer (200mM Tris (pH7.5), 25mM EDTA, 300mM NaCl and 2% (w/v) SDS). Proteinase K (Sigma, Cat No. P2308) was added to a final concentration of 200µg/ml and the mixture incubated at 37°C for 30 min.

The preparation was extracted with an equal volume of phenol/chloroform, the aqueous phase removed and 2.5 vol ethanol added and mixed. This solution was then stored at -20°C overnight. RNA was collected by centrifugation (4000 rpm, 30 min at 4°C in a bench top centrifuge, Sorval RT6000B), the supernatant decanted and the pellet dried in a vacuum dessicator after which it was dissolved in 250 µl diethylpyrocarbonate (DEPC)-treated water (prepared as described in Maniatis, referenced above). The RNA content was measured by spectrophotometry and the concentration calculated assuming an absorbance at 260nm of 1 = 40 µg/ml.

7.2 Preparation of first strand variable region cDNA

A number of methods for the synthesis of cDNA are reviewed in Maniatis (Chapter 8). The oligonucleotide primers used were mainly based on those proposed by Marks et al. J. Mol. Biol (1991) 222, 581-597. The cDNA in this case was prepared as described below. RNA (5mg) was mixed in a microcentrifuge tube with 10 µl 5x reverse transcriptase buffer [250mM Tris (pH8.3), 40mM $MgCl_2$ and 50mM DTT], 1µl forward primer (25 pM), 10µl 1.25mM dNTPs, 5µl 10 mM DTT, 0.5µl RNAguard (Pharmacia) to which DEPC-treated H2O was added to obtain a volume of 50µl. The reaction mix was heated to 70°C for 10 min and then cooled slowly to 37°C, after which 100 u (0.5µl) M-MLV reverse transcriptase (Pharmacia Cat. No. 27-0925-01) were added and the reaction incubated at 37°C for 1 h. The forward primer used for the generation of the light chain cDNA was oligonucleotide CK2FOR (SEQ ID NO: 1) which is designed to hybridise to the CK constant region of murine kappa light chain genes. For the heavy chain cDNA the forward primer CG1FOR (SEQ ID NO: 2) was used which hybridises to the CH1 constant domain of murine IgG1.

7.3 Amino acid sequencing

The heavy and light chains of the 806.077 antibodies were isolated by SDS-PAGE and Western blotting and submitted for N-terminal amino acid sequencing. The results showed that the N-terminus of the light chain was chemically blocked, however, sequence data was obtained for the first 34 N-terminal residues of the heavy chain (SEQ ID NO: 3).

On the basis of this amino acid sequence a specific DNA back primer was designed for 806.077 heavy chain variable region PCR. This primer was called SP1back (SEQ ID NO: 7).

7.4 Isolation of antibody gene fragments by PCR

Isolation of 806.077 heavy and light chain variable region genes was performed using the cDNA prepared as described above as template. General reaction conditions were as follows.

To 5µl of the cDNA reaction was added 5µl dNTPs (2.5mM), 5µl 10x Enzyme buffer (500mM KCl, 100mM Tris (pH8.3), 15mM $MgCl_2$ and 0.1% gelatin), 1µl of 25pM/µl back primer, 1µl of 25pM/µl forward primer, 0.5µl thermostable DNA polymerase and DEPC-treated water to obtain a volume of 50µl. The PCR conditions were set for 25 cycles at 94°C for 90s; 55°C for 60s; 72°C for 120s, ending the last cycle with a further 72°C for 10 min incubation.

Using the general reaction conditions, the forward primer used for the generation of the light chain cDNA was oligonucleotide CK2FOR (SEQ ID NO: 1) and the for the heavy chain cDNA oligonucleotide CG1FOR (SEQ ID NO: 2). A number of reactions using a variety of different back primers were performed for both the heavy and light chains to obtain desired specific PCR products.

In the case of the 806.077 light chain, on analysis a specific PCR product was obtained using the back primers VK1back (SEQ ID NO: 4) and VK4back (SEQ ID NO: 5). Similarly specific PCR products were obtained for the heavy chain using VH1back (SEQ ID NO: 6) and SP1back primers (SEQ ID NO: 7). Reaction products were analysed on a 2% agarose gel. Products of the expected size, were excised and the DNA purified.

7.5 Cloning of the PCR products into Bluescript KS+ vector

For each antibody fragment, both the 5' region (back primer) oligonucleotide and the 3' region (forward primers) introduced a restriction site. The discrete PCR products were for both the VH and VK PCR reactions were therefore able to be cloned into the Bluescript vector KS+ (Stratagene Cloning Systems) via the appropriate enzyme restriction sites using standard DNA manipulation methods (e.g. PCR products VH1back/CG1For was cloned via PstI/HindIII and VK4back/CK2For via SacI/HindIII). DNA was prepared from the clones obtained and rigorous sequencing of at least 12 clones of each construct performed using automated fluorescent sequencing equipment (Applied Biosystems). The sequences were

reviewed, compared and aligned using suitable computer software. Consensus sequences for both the VH and VK genes were obtained and subsequently translated to their corresponding amino acid sequence.

The DNA and amino acid sequences obtained for the 806.077 light chain variable (VK) region are described in SEQ ID NO: 8 and SEQ ID NO: 9 respectively. The DNA and amino acid sequences obtained for the 806.077 heavy chain variable (VH) region are described in SEQ ID NO: 10 and SEQ ID NO: 11 respectively. A clone containing the light chain was designated VK4, and a clone containing the heavy chain sequnece was designated VH14A.

Example 8

Construction of chimaeric light chain and heavy chain Fd genes

The heavy and light chain genes which had been cloned into Bluescript (VK4 and VH14A in Example 7) were isolated by PCR using primers which allowed specific amplification of only the variable region the appropriate genes but also introduced new unique enzyme restriction sites. These restriction sites enabled the variable region gene fragments to be cloned in frame with DNA fragments coding for both the appropriate antibody signal sequences and human constant regions. The signal and constant region sequences for the light and heavy chain Fd had each been previously cloned into pNG3 and pNG4, derivatives of the pSG5 Eukaryotic plasmid expression vector.

The vector pNG3 was prepared as follows. Plasmid pSG5 (Stratagene, Cat. No. 216201) was digested with SalI and XbaI to remove the existing SV40 promoter and polylinker sequence. A new polylinker was introduced by use of oligonucleotides SEQ NOS: 34 and 35 which were hybridised and cloned into the SalI and XbaI cut pSG5 plasmid to give plasmid pNG1. The pNG1 plasmid was cut with BglII and HindIII and the BglII-HindIII CMV promoter fragment from pcDNA3 (Invitrogen, Cat. No. V790-20) cloned into this site to give plasmid pNG2. Finally, the polyA region from pSG5 was isolated by PCR as described in Example 7, section 7.4 but using oligonucleotide sequences SEQ ID NOS: 36 and 37 with plasmid pSG5. The PCR product was cut with XmaI and BamHI, purified by electrophoresis on a 2% agarose gel, isolated (e.g. with GENECLEAN, see example 7) then ligated into the XmaI-BamHI cut pNG2 plasmid to give pNG3.

The pNG4 vector was prepared as follows. The pNG3 vector was further modified such that the SacI restriction enzyme recognition site in the cloned CMV promoter fragment was corrupted by changing the DNA sequence. This was achieved by the use of a two step PCR mutagenesis reaction using the pNG3 vector as a template. The PCR used two complementary oligonucleotide primers (SEQ ID NOS: 38 and 39) to mutate the Sac I recognition sequence and 2 flanking primers (SEQ ID NOS: 40 and 41) for product amplification. Two Primer pairs (SEQ ID NOS: 38 and 41) and (SEQ ID NOS: 39 and 40) were used in a standard PCR reaction (as described in Example 7, section 7.4) to obtain the initial 2 PCR products, which were isolated by electrophoresis on 2% agarose gels. Equimolar amounts of each product were mixed and reamplified using the flanking primers (SEQ ID NOS: 40 and 41) under the standard PCR reaction conditions to splice together and amplify the final PCR product. This product was subsequently digested with the restriction enzymes NcoI and HindIII and cloned into the appropriately restricted and prepared pNG3 vector such that the mutated (SacI site minus) fragment replaced the original pNG3 NcoI-Hind III (SacI site plus) fragment. This new vector was named pNG4.

A clone of the 806.077 murine light chain in the Bluescript KS+ vector (VK4) was taken and amplified using the oligonucleotide primers 077VK-UP (SEQ ID NO: 12) and 077VK-DOWN (SEQ ID NO: 13). Similarly a 806.077 heavy chain clone (VH14A) was amplified using 077VH-UP (SEQ ID NO: 14) and 077VH-DOWN (SEQ ID NO:15). The PCR was performed as follows: To 100ng of plasmid DNA was added 5µl dNTPs (2.5mM), 5µl 10x Enzyme buffer (see above), 1µl of 25pM/µl back primer, 1µl of 25pM/µl forward primer, 0.5µl thermostable DNA polymerase and DEPC-treated water to obtain a volume of 50µl. The PCR conditions were set for 15 cycles at 94°C for 90s; 55°C for 60s; 72°C for 120s, ending the last cycle with a further 72°C for 10 min incubation. The products were analysed on a 2% agarose gel. The DNA was purified and the DNA fragment digested with the relevant restriction enymes in preparation for subsequent vector cloning.

For secretion of antibody light chain, a double stranded DNA cassette which contained both the information for a Kozak recognition sequence and a light chain signal sequence was designed. The cassette consisted of two individual oligonucleotides (SEQ ID NOS: 42 and 43) which were hybridised and subsequently cloned between cloned between the HindIII and SacII restriction site of the pNG3 plasmid (which had been appropriately restricted and isolated using standard methodology) to create the vector pNG3-Vkss. The DNA sequence of

SEQ ID NO: 46, which contains the sequence for the human light chain kappa constant region, was digested with XmaI and XhoI and inserted between the XhoI and XmaI cut pNG-Vkss plasmid to give the vector pNG3-Vkss-HuCk (NCIMB no. 40798). Furthermore, a neomycin resistance gene expression cassette was cloned into pNG3-Vkss-HuCk (from the pSG5 plasmid variant pSG5-Neo vector, supplied from S.Green, Zeneca Pharmaceuticals; alternative sources include vectors such as pMC1neo, Stratagene cat. no. 213201). The neomycin resistance gene expression cassette was cloned as an XbaI fragment and cloned into the XbaI site of the pNG3-Vkss-HuCk and the orientation was checked using restriction enzyme digestion. This gave rise to the plasmid pNG3-Vkss-HuCk-Neo (NCIMB 40799). The light chain gene sequence described above was inserted, in frame, by cloning directly between the SacII and XhoI sites of the pNG3-Vkss HuCk-neo vector. The PCR fragment obtained for the light chain gene was digested with SacII and XhoI restriction enzymes and cloned into the similarly restricted expression vector containing the VK signal and HuCK constant region coding sequences. The chimaeric 806.077 light chain sequence created is shown in SEQ ID NOS: 16 and 17.

Similarly, for secretion of antibody heavy chain, a double stranded DNA cassette which contained both the information for a Kozak recognition sequence and a heavy chain signal sequence was designed. The cassette consisted of two individual oligonucleotides (SEQ ID NOS: 44 and 45) which were hybridised and subsequently cloned between cloned between the HindIII and EcoRI restriction site of the pNG4 plasmid (which had been appropriately restricted and isolated using standard methodology) to create the vector pNG4-VHss. Heavy chain gene sequences could thus be inserted. in frame, by cloning directly between the EcoRI and SacI sites of the pNG4-VHss vector. The DNA sequence of SEQ ID NO: 47, which contains the coding sequence for human heavy chain IgG2CH1' constant region (SEQ ID NOS: 22 and 23) was digested with SacI and XmaI and cloned into pNG4-VHss cut with SacI and XmaI to give the vector pNG4-VHss-HuIgG2CH1' (NCIMB no. 40797). The PCR fragment obtained for the heavy chain gene was digested with EcoRI and SacI restriction enzymes and cloned into the similarly restricted expression vector pNG4-VHss-HuIgG2CH1' containing the VH signal and HuIgG2 CH1' constant region coding sequences. The chimaeric 806.077 HuIgG2 Fd chain sequence created is shown in SEQ ID NOS: 18 and 19.

In some instances it may be preferable to use other classes of chimaeric heavy chain Fd constructs. To this end, variants of the heavy chain vector are made containing HuIgG1CH1' (SEQ ID NOS: 20 and 21) or HuIgG3CH1' (SEQ ID NOS: 24 and 25) which are substituted for the HuIgG2CH1' (SEQ ID NOS: 22 and 23) gene.

The sequences shown in SEQ ID NOS: 46 and 47 are prepared by a variety of methods including those described by Edwards (1987) Am. Biotech. Lab. 5, 38-44, Jayaraman et al. (1991) Proc. Natl. Acad. Sci. USA 88, 4084-4088, Foguet and Lubbert (1992) Biotechniques 13, 674-675 and Pierce (1994) Biotechniques 16, 708. Preferably, the sequences shown in SEQ ID NOS: 46 and 47 are prepared by a PCR method similar to that described by Jayaraman et al. (1991) Proc. Natl. Acad. Sci. USA 88, 4084-4088.

Once the individual heavy and light chain sequences were constructed a heavy chain Fd gene expression cassette (including both promoter and gene was excised as a BglII/SalI fragment and cloned between into the BamHI/SalI sites of the light chain vector to produce a co-expression vector construct. This construct was transfected into NS0 myeloma cells (ECACC No. 85110503) via standard techniques of electroporation and transfectants selected for the property of G418 resistance, a trait which is carried as a selectable marker on the expression plasmid construct.

Alternatively the complete heavy chain Fd and light chain genes may simply be excised from their respective vectors as HindIII/XmaI fragments and subsequently cloned into other expression vector systems of choice.

Example 9

Hybridization test of nucleic acid variations of specific nucleic acid sequences

9.1 Hybridisation Test

A method for detecting variant nucleic acids containing sequences related to specific 806.077 antibody sequences is described. These variant nucleic acids may be present in a variety of forms such as the DNA from bacterial colonies or the DNA/RNA from eukaryotic cells fixed on to a membrane as described above in the screening of a cDNA library or as fragments of purified nucleic acid separated by gel electrophoresis and then transfered to a suitable membrane as for the techniques of Northern (Maniatis et al, Chapter 7, p39) or Southern (Maniatis, chapter 9, p31) hybridisation.

9.2 Hybridisation probe

Hybridisation probes may be generated from any fragment of DNA or RNA encoding the specific 806.077 antibody nucleic sequence of interest, more specifically from the variable region, particularly the region encoding CDR3 of this region. A synthetic oligonucleotide or its complementary sequence can be used as a specific probe for the CDR3 encoding region.

A hybridisation probe can be generated from a synthetic oligonucleotide by addition of a radioactive 5' phospate group from [γ-^{32}P]ATP by the action of T4 polynucleotide kinase. 20 pmoles of the oligonucleotide are added to a 20µl reaction containing 100mM Tris, pH7.5 , 10mM $MgCl_2$, 0.1mM spermidine, 20mM dithiothreitol (DTT), 7.55µM ATP, 55µCi [γ-^{32}P]ATP and 2.5u T4 polynucleotide kinase (Pharmacia Biotechnology Ltd, Uppsala, Sweden). The reaction is incubated for 30 minutes at 37°C and then for 10 minutes at 70°C prior to use in hybridisation. Methods for the generation of hybridisation probes from oligonucleotides (chapter 11) or from DNA and RNA fragments (chapter 10) are given in Maniatis. A number of proprietary kits are also available for these procedures.

9.3 Hybridisation conditions

Filters containing the nucleic acid are pre-hybridised in 100ml of a solution containing 6x SSC, 0.1%SDS and 0.25% dried skimmed milk (Marvel™) at 65°C for a minimum of 1 hour in a suitable enclosed vessel. A proprietary hybridisation apparatus such as model HB-1 (Techne Ltd) provides reproducible conditions for the experiment.

The pre-hybridisation solution is then replaced by 10ml of a probe solution containing 6xSSC, 0.1% SDS, 0.25% dried skimmed milk (e.g. Marvel™) and the oligonucleotide probe generated above. The filters are incubated in this solution for 5 minutes at 65°C before allowing the temperature to fall gradually to below 30°C. The probe solution is then discarded and the filters washed in 100ml 6xSSC, 0.1% SDS at room temperature for 5 minutes. Further washes are then made in fresh batches of the same solution at 30°C and then in 10°C increments up to 60°C for 5 minutes per wash.

After washing, the filters are dried and used to expose an X-ray film such as Hyperfilm™ MP (Amersham International) at -70°C in a light-tight film cassette using a fast tungstate intensifying screen to enhance the photographic image. The film is exposed for a suitable period (normally overnight) before developing to reveal the photographic image of the radio-active areas on the filters. Related nucleic acid sequences are identified by the

presence of a photographic image compared to totally unrelated sequences which should not produce an image. Generally, related sequences will appear positive at the highest wash temperature (60°C). However, related sequences may only show positive at the lower wash temperatures (50, 40 or 30°C).

These results will also depend upon the nature of the probe used. Longer nucleic acid fragment probes will need to be hybridised for longer periods at high temperature but may remain bound to related sequences at higher wash temperatures and/or at lower salt concentrations. Shorter, mixed or degenerate oligonucleotide probes may require less stringent washing conditions such as lower temperatures and/or higher Na^+ concentrations. A discussion of the considerations for hybridisation protocols is provided in Maniatis (chapter 11).

Example 10

Pharmaceutical compositions

The following illustrates representative pharmaceutical dosage forms containing 806.077 antibody which may be used for therapy in combination with a suitable prodrug.

Injectable solution for ADEPT

A sterile aqueous solution, for injection, containing per ml of solution:

806.077 antibody - CPG2 conjugate	1.0mg
Sodium acetate trihydrate	6.8mg
Sodium chloride	7.2mg
Tween 20	0.05mg

A typical dose of conjugate for adult humans is 30mg followed 3 days later by three 1g doses of prodrug administered at hourly intervals. Suitable CPG2 conjugates are any one of those conjugates described in Examples 105 and 106. Conjugates with HCPB may replace the CPG2 conjugate in the table. Suitable HCPB conjugates are any one of those conjugates described in Examples 48-101.

Injectable solution for Tumour Immunotherapy

A sterile aqueous solution, for injection, containing per ml of solution:

806.077 antibody - B7 conjugate	1.0mg
Sodium acetate trihydrate	6.8mg
Sodium chloride	7.2mg
Tween 20	0.05mg

A typical dose of conjugate for adult humans is 30mg. A suitable conjugate is described in Example 104.

Example 11

Construction of Initial 806.077 humanised antibody heavy and light chain variable region genes

Firstly an overview of the humanisation strategy is set out in the following text. The purpose of antibody humanisation is to combine the binding site of a non-human antibody into the supporting framework of a human antibody while maintaining the characteristic antigen binding affinity and specificity properties of the parent antibody. The feasibility of such antibody engineering is a consequence of the close sequence and structural homology of immunoglobulins from different mammalian species.

In its most basic form the approach involes the transfer of the six hypervariable regions or complementarity determing regions (CDRs) from one antibody Fv region to another, as first described in Jones etal Nature (1986) 321 522-525. However, experience has shown that in addition to the CDRs it is often necessary that amino acids in the antibody framework also need to be transferred for the process to be successful since such residues sometimes appear to contact and influence the conformation of the CDR loops.

In the case of the 806.077 antibody an "Initial" humanised version of the antibody was made which comprises the six murine CDRs and a number of framework residue substitutions. This construct was used as a template from which further variants (Examples 12-47) were made by introducing additional "murine" residue substitutions. The rest of this Example describes the Initial humanised construct in detail.

The human antibody heavy chain variable region NEWM (Poljak,R.J et al (1974) PNAS 71 3440-3444) and the light chain kappa variable region REI (Palm, W and Hilschmann, N. Z. (1975) Physiol. Chem. **356** 167-191 were chosen to form the acceptor human antibody framework. Numerous examples of successful humanisations using this Fv framework have been described in the literature and the 3 dimensional structure of these two protein domains has been solved. Based on comparison of the murine 806.077 heavy and light chain variable region protein sequences with their closest related Kabat murine subgroup concensus sequences (and the individual sequence members) and the human NEWM and REI protein sequences, individual DNA sequences were designed to encode for the Initial humanised antibody which incorporated the murine CDRs and any additional framework substitutions considered to be of importance.

The murine 806.077 CDR sequences incorporated are described in SEQ ID NOs: 26; 27 and 28 for the light chain variable region and are found at positions 24-34 (CDR1), 50-56 (CDR2) and 89-97 (CDR3) repectively. The CDRs incorporated in the heavy chain variable region are described in SEQ ID NOs: 29, 31 and 32 being at positions 31-35 (CDR1), 50-65 (CDR2), 95-102 (CDR3) respectively (using Kabat nomenclature). In the heavy chain variable region the additional changes V24A; S27F; T28N; F29I; S30K;.V71A; A92H; R93V (Kabat nomenclature) were made to the NEWM framework and in the light chain variable region no additional framework changes were made.

Individual synthetic DNA sequences were designed to encode for the initial version of the 806.077 humanised antibody heavy (806.077HuVH1) and light chain (806.077HuVK1) variable regions in which the CDRs and any additional framework residue changes were incorporated. The antibody variable gene sequences shown in SEQ ID NOS: 48 and 53 may be prepared by a variety of methods including those described by Edwards (1987) Am. Biotech. Lab. 5, 38-44, Jayaraman et al. (1991) Proc. Natl. Acad. Sci. USA 88, 4084-4088, Foguet and Lubbert (1992) Biotechniques 13, 674-675 and Pierce (1994) Biotechniques 16, 708. Preferably, the DNA sequences shown in SEQ ID NOS: 48 and 53 are prepared by a PCR method similar to that described by Jayaraman et al. (1991) Proc. Natl. Acad. Sci. USA 88, 4084-4088.

The humanised 806.077 antibody variable light chain gene sequence (SEQ ID NO: 49 and 50) was inserted, in frame, by cloning into the pNG3-Vkss-HuCK-Neo (NCIMB no. 40799) expression vector. To achieve this, the synthetic PCR DNA fragment encoding the

humanised variable light chain gene (SEQ ID NO: 48) was digested with SacII and XhoI restriction enzymes and cloned into the similarly restricted pNG3-Vkss-HuCK-Neo vector which contained the VK signal sequence and HuCK constant region coding sequences. The DNA and protein sequence of completed humanised 806.077 light chain sequence (806.077HuVK1-HuCK) produced, together with its signal sequence, are shown in SEQ ID NOS: 51 and 52 respectively and the vector named pNG3-Vkss-806.077HuVK1-HuCK-Neo.

Similarly, for the humanised antibody heavy chain, the humanised variable heavy chain gene sequence SEQ ID NO: 54 and 55 was inserted, in frame, by cloning directly into the pNG4-VHss-HuIgG2CH1' (NCIMB no. 40797) expression vector. To achieve this, the synthetic PCR fragment obtained for the humanised heavy chain gene (SEQ ID NOS: 53) was digested with EcoRI and SacI restriction enzymes and cloned into the similarly restricted pNG4-VHss-HuIgG2CH1' vector which contained the VH signal sequence and HuIgG2 CH1' constant region coding sequences. The DNA and protein sequence of completed humanised 806.077 Fd heavy chain sequence (806.077HuVH1-HuIgG2 Fd) produced, together with its signal sequence, are shown in SEQ ID NOS: 56 and 57 respectively and the vector named pNG4-VHss-806.077HuVH1-HuIgG2 CH1'.

The Initial humanised antibody construct was produced by constructing a co-expression plasmid containing both 806.077 HuVK1 light chain and 806.077 HuVH1 heavy chain variable region antibody genes. The plasmid pNG3-Vkss-806.077HuVK1-HuCK-Neo vector, which contains the humanised light chain variable region HuVK1 (SEQ ID NOS: 49 and 50) was digested using the restriction enzymes BamHI and SalI and the vector run on a 1% agarose gel, the vector band was excised and purified. The plasmid pNG4-VHss-806.077HuVH1-HuIgG2 CH1' (which contains the humanised 806.077HuVH1 heavy chain variable region (SEQ ID NOS: 56 and 57)) was digested using the restriction enzymes BglII and SalI, the reaction run on a 2% agarose and the fragment band excised and purified. The DNA fragment recovered was subsequently ligated into the prepared pNG3-Vkss-806.077HuVK1-HuCK-Neo vector to produce clones of the desired HuVH1/HuVK1 co-expression vector.

These constructs were transfected into NS0 myeloma cells (ECACC No. 85110503) via standard techniques of electroporation and transfectants selected for the property of G418 antibiotic resistance. The clones obtained were tested for both antibody expression in the anti-human antibody Fd ELISA and CEA binding ELISA assays described below.

For the CEA ELISA each well of a 96 well immunoplate (NUNC MAXISORB™) was coated with 50ng CEA in 50 mM carbonate/bicarbonate coating buffer pH9.6 (buffer capsules - Sigma C3041) and incubated at 4°C overnight. The plate was washed three times with PBS+0.05% Tween 20 and then blocked 150µl per well of 1% BSA in PBS + 0.05% Tween 20 for 1 hour at room temperature. The plate was washed as previously described, 100µl of test sample added per well and incubated at room temperature for 2 hours. Again the plate was washed three times with PBS+0.05% Tween 20, 100µl per well of a 1/500 dilution of HRPO-labelled goat anti-human kappa antibody (Sigma A 7164) was added, in 1% BSA in PBS-Tween 20 and incubated at room temperature on a rocking platform for at least 1 hour. The plate was washed as before and then once more with PBS. To detect binding add 100µl per well developing solution (one capsule of phosphate-citrate buffer - Sigma P4922 - dissolved in 100 mls H_2O to which is added one 30 mg tablet *o*-phenylenediamine dihydrochloride - Sigma P8412) and incubated for up to 15 minutes. The reaction was stopped by adding 75µl 2M H_2SO_4, and absorbance read at 490nm.

In the anti-human antibody Fd ELISA, each well of a 96 well immunoplate was coated with 1.2µg sheep anti-human Fd antibody (Binding Site PC075) in 50 mM carbonate/-bicarbonate coating buffer pH9.6 (buffer capsules - Sigma C3041) and incubated at 4°C overnight. The plate was washed three times with PBS+0.05% Tween 20 and then blocked with 150µl per well of 1% BSA in PBS + 0.05% Tween 20 for 1 hour at room temperature. The plate was washed as previously described, 100µl of test sample added per well and incubated at room temperature for 2 hours. Again the plate was washed three times with PBS+0.05% Tween 20, 100µl per well of HRPO-labelled goat anti-human kappa antibody (Sigma A 7164) was added in 1% BSA in PBS-Tween 20 and incubated at room temperature on a rocking platform for at least 1 hour. Wash plate as before and then once more with PBS. To detect binding, developing solution etc was added as described above for the CEA binding assay.

The clones found to show the best expression and CEA binding levels were selected for further expansion into 24 well plates and re-tested. The best clone according to these assay criteria was selected and expanded such that a one litre production was undertaken , which was seeded using a 1:10 dilution of a confluently grown culture (i.e. 100mls into 900mls of fresh culture medium) and the grown for a further 14 days. The human $F(ab')_2$ antibody fragment was then purified from the culture supernatant as described in Example 102.

Examples 12-38

Further combinations of humanised heavy and light chain variable region gene variants: Construction of 806.077 Humanised heavy and light variable region variants.

The Initial humanised 806.077 variable region genes were also used for the subsequent construction of further gene constructs which contained additional murine framework residues. Modifications of the gene sequences were achieved (in the majority of cases) by cassette mutagenesis. In this technique part of the original gene was removed via restriction with two appropriate unique enzymes from the complete plasmid vector and then replaced by a double stranded DNA cassette (consisting of two complementary oligonucleotides hybridised together to form a DNA fragment with the appropriate cohesive ends) by direct ligation into the prepared plasmid thus reconstituting the gene but now containing desired DNA changes. Further combinations of mutations within either the heavy or light chain could be also be produced by simple DNA fragment exchanges between the appropriate variants by utilising the available unique restriction enzyme sites.

Three further variants of the humanised light chain variable region were produced in addition to the original sequence HuVK1 (SEQ ID NO: 49 and 50) and these were called HuVK2, HuVK3 and HuVK4 repectively. The light chain variable region variant HuVK2 was a modification of the original HuVK1 coding sequence in order to produce the amino acid change M4L (Kabat nomenclature), with the gene (SEQ ID NO: 49) being mutated by cassette mutagenesis. The plasmid pNG3-Vkss-806.077HuVK1-HuCK-Neo (which contains the complete humanised light chain (SEQ ID NOS: 49 and 50) was digested using the restriction enzymes SacII and NheI. The digest was then loaded on a 2 % agarose gel and the excised fragment separated from the remaining vector. The vector DNA was then excised from the gel, recovered and stored at -20°C until required. Two oligonucleotides (containing the desired base changes) were designed and synthesised (SEQ ID NO: 58 and 59). These two oligonucleotides were hybridised by adding 200 pmoles of each oligonucleotide into a total of 30 µl of H_2O, heating to 95°C and allowing the solution to cool slowly to 30°C. 100pmoles of the annealed DNA product was then ligated directly into the previously prepared vector. This DNA "cassette" exchange produced the desired HuVK2 DNA and protein sequence (SEQ ID NO: 60 and 61) already in place in the expression vector pNG3-Vkss-806.077HuVK2-HuCK-Neo.

Similarly, HuVK3 with the amino acid changes D1Q; Q3V; M4L (Kabat nomenclature) was constructed using synthetic oligonucleotides (SEQ ID NO: 62 and 63) to produce the desired HuVK3 DNA and protein sequence (SEQ ID NO: 64 and 65) again already in place in the expression vector pNG3-Vkss-806.077HuVK3-HuCK-Neo.

The light chain variable region variant HuVK4 was produced by a different technique, as there were not unique restriction enzyme sites available close to the mutation site. HuVK4, with the amino acid change L47W, was produced by a PCR mutagenesis technique. The vector pNG3-806.077HuVK1-HuVK-Neo was used as the template for two PCR reactions (94°C, 90sec; 55°C, 60 sec; 72°C, 120 sec for 15 cycles, all buffers, etc., as previously described). Reaction A used the synthetic oligonucleotide sequence primers SEQ ID NOS: 66 and 67 and reaction B the synthetic oligonucleotide sequence primers SEQ ID NOS: 68 and 69. The products of these PCR reactions (A and B) were fragments of length 535 base pairs and 205 base pairs respectively. These reaction products were run on a 2 % agarose gel and separated from any background products. Bands of the expected size were excised from the gel and recovered. Mixtures of varying amounts of the products A and B were made and PCR reactions performed using the synthetic oligonucleotides SEQ ID NOS: 66 and 68. The resulting product (ca.700 base pairs) was digested with the restriction enzymes SacII and XhoI and the cleavage products separated on a 2% agarose gel. The band of the expected 310 base pairs size was excised from the gel and recovered. This fragment was then ligated into the vector pNG3-806.077HuVK1-HuVK-Neo vector (which had been previously cut with the restriction enzymes SacII/XhoI and subsequently isolated) and thus created the desired HuVK4 DNA and protein sequence (SEQ ID NO: 70 and 71) within the expression vector pNG3-Vkss-806.077HuVK4-HuCK-Neo.

Six further variants of the humanised heavy chain variable region were produced in addition to the original HuVH1 sequence (SEQ ID NO: 54 and 55) and these were called HuVH2 to HuVK7 respectively. The heavy chain variable region variant HuVH2 was a modification of the original HuVH1 coding sequence in order to produce the amino acid change G49A (Kabat nomenclature), with the gene (SEQ ID NO: 54) being mutated by cassette mutagenesis. The plasmid pNG4-VHss-806.077HuVH1-HuIgG2 CH1' (which contains the complete humanised, IgG2 heavy chain Fd (SEQ ID NOS: 56 and 57) was digested using the restriction enzymes StuI and NotI. The digest was then loaded on a 2 % agarose gel and the excised fragment separated from the remaining vector. The vector DNA

was then excised from the gel, recovered and stored at -20°C until required. Two oligonucleotides were designed, synthesised (SEQ ID NO: 72 and 73), hybridised and the product ligated directly into the previously prepared vector. This DNA "cassette" exchange produced the desired HuVH2 DNA and protein sequence (SEQ ID NO: 74 and 75) already in place in the expression vector pNG4-VHss-806.077HuVH2-HuIgG2 CH1'.

Similarly, HuVH3 with the amino acid changes T73S; F78A (Kabat nomenclature) was constructed using synthetic oligonucleotides (SEQ ID NO: 76 and 77), however, in this case, the vector pNG4-VHss-806.077HuVH1-HuIgG2 CH1' was digested using the restriction enzymes NotI and SacII. The synthetic DNA cassette was ligated directly into the previously prepared vector to produce the desired HuVH3 DNA and protein sequence (SEQ ID NO: 78 and 79) in the expression vector pNG4-VHss-806.077HuVH3-HuIgG2 CH1'.

HuVH4 with the amino acid changes G49A; T73S; and F78A (Kabat nomenclature) combines the HuVH2 (SEQ ID NO: 74 and 75) and HuVH3 (SEQ ID NO: 78 and 79) variants. This was achieved by digesting the pNG4-VHss-806.077HuVH3-HuIgG2 CH1' vector with the enzymes NotI and NheI and isolating the ca. 200 base pairs NotI/NheI restriction fragment after separation on a 2% agarose gel. The fragment was recovered and subsequently ligated into the pNG4-VHss-806.077HuVH2-HuIgG2 CH1' vector (which had been digested with the same Not I and NheI restriction enzymes and the vector fragment purified). The resulting clones contained the desired HuVH4 DNA and protein sequence ((SEQ ID NO: 80 and 81) in the expression vector pNG4-VHss-806.077HuVH4-HuIgG2 CH1'.

HuVH5 with the amino acid changes V67A (Kabat nomenclature) was constructed using synthetic oligonucleotides (SEQ ID NO: 82 and 83). Again, the vector pNG4-VHss-806.077HuVH1-HuIgG2 CH1' was digested using the restriction enzymes NotI and SacII. The synthetic DNA cassette was ligated directly into the previously prepared vector to produce the desired HuVH5 DNA and protein sequence (SEQ ID NO: 84 and 85) in the expression vector pNG4-VHss-806.077HuVH5-HuIgG2 CH1'.

HuVH6 with the amino acid changes V67A;T73S and F78A (Kabat nomenclature) was constructed using synthetic oligonucleotides (SEQ ID NO: 86 and 87) and for this mutant the vector pNG4-VHss-806.077HuVH1-HuIgG2 CH1' was digested using the restriction enzymes NotI and SacII. The synthetic DNA cassette was ligated directly into the

previously prepared vector to produce the desired HuVH6 DNA and protein sequence (SEQ ID NO: 88 and 89) in the expression vector pNG4-VHss-806.077HuVH6-HuIgG2 CH1'.

HuVH7 with the amino acid changes G49A; V69A; T73S; and F78A (Kabat nomenclature) combines the HuVH2 (SEQ ID NO: 74 and 75) and HuVH6 (SEQ ID NO: 88 and 89) variants. This was achieved by digesting the pNG4-VHss-806.077HuVH6-HuIgG2 CH1' vector with the enzymes NotI and NheI and isolating the ca. 200 base pairs NotI/NheI restriction fragment after separation on a 2% agarose gel. The fragment was recovered and ligated into the pNG4-VHss-806.077HuVH2-HuIgG2 CH1' vector (which had been digested with the same Not I and NheI restriction enzymes and the vector fragment purified). The resulting clones contained the desired HuVH7 DNA and protein sequence (SEQ ID NO: 90 and 91) in the expression vector pNG4-VHss-806.077HuVH7-HuIgG2 CH1'.

Combinations of such humanised heavy and light chain variable gene variants were made by excising the heavy chain Fd gene variant expression cassette (including both promoter and gene excised as a BglII/SalI fragment) and cloning this fragment into the BamHI/SalI sites of the light chain variant vector to produce a co-expression vector construct. A listing of the possible combinantions of variants based on the humanised heavy and light chain variants previously described is shown in the table below.

Table- Combinations of humanised heavy and light chain variable region variants.

Example No.	Heavy chain variable region	SEQ ID NOS:	Light chain variable region	SEQ ID NOS:	Co-expression Plasmid Vector
11	HuVH1	54 and 55	HuVK1	49 and 50	pNG 806HuVH1/HuVK1/HuIgG2
12	HuVH1	54 and 55	HuVK2	60 and 61	pNG 806HuVH1/HuVK2/HuIgG2
13	HuVH1	54 and 55	HuVK3	64 and 65	pNG 806HuVH1/HuVK3/HuIgG2
14	HuVH1	54 and 55	HuVK4	70 and 71	pNG 806HuVH1/HuVK4/HuIgG2
15	HuVH2	74 and 75	HuVK1	49 and 50	pNG 806HuVH2/HuVK1/HuIgG2
16	HuVH2	74 and 75	HuVK2	60 and 61	pNG 806HuVH2/HuVK2/HuIgG2
17	HuVH2	74 and 75	HuVK3	64 and 65	pNG 806HuVH2/HuVK3/HuIgG2
18	HuVH2	74 and 75	HuVK4	70 and 71	pNG 806HuVH2/HuVK4/HuIgG2
19	HuVH3	78 and 79	HuVK1	49 and 50	pNG 806HuVH3/HuVK1/HuIgG2
20	HuVH3	78 and 79	HuVK2	60 and 61	pNG 806HuVH3/HuVK2/HuIgG2
21	HuVH3	78 and 79	HuVK3	64 and 65	pNG 806HuVH3/HuVK3/HuIgG2

22	HuVH3	78 and 79	HuVK4	70 and 71	pNG 806HuVH3/HuVK4/HulgG2
23	HuVH4	80 and 81	HuVK1	49 and 50	pNG 806HuVH4/HuVK1/HulgG2
24	HuVH4	80 and 81	HuVK2	60 and 61	pNG 806HuVH4/HuVK2/HulgG2
25	HuVH4	80 and 81	HuVK3	64 and 65	pNG 806HuVH4/HuVK3/HulgG2
26	HuVH4	80 and 81	HuVK4	70 and 71	pNG 806HuVH4/HuVK4/HulgG2
27	HuVH5	84 and 85	HuVK1	49 and 50	pNG 806HuVH5/HuVK1/HulgG2
28	HuVH5	84 and 85	HuVK2	60 and 61	pNG 806HuVH5/HuVK2/HulgG2
29	HuVH5	84 and 85	HuVK3	64 and 65	pNG 806HuVH5/HuVK3/HulgG2
30	HuVH5	84 and 85	HuVK4	70 and 71	pNG 806HuVH5/HuVK4/HulgG2
31	HuVH6	88 and 89	HuVK1	49 and 50	pNG 806HuVH6/HuVK1/HulgG2
32	HuVH6	88 and 89	HuVK2	60 and 61	pNG 806HuVH6/HuVK2/HulgG2
33	HuVH6	88 and 89	HuVK3	64 and 65	pNG 806HuVH6/HuVK3/HulgG2
34	HuVH6	88 and 89	HuVK4	70 and 71	pNG 806HuVH6/HuVK4/HulgG2
35	HuVH7	90 and 91	HuVK1	49 and 50	pNG 806HuVH7/HuVK1/HulgG2
36	HuVH7	90 and 91	HuVK2	60 and 61	pNG 806HuVH7/HuVK2/HulgG2
37	HuVH7	90 and 91	HuVK3	64 and 65	pNG 806HuVH7/HuVK3/HulgG2
38	HuVH7	90 and 91	HuVK4	70 and 71	pNG 806HuVH7/HuVK4/HulgG2

Analogously with Example 11, Example 14 was produced by constructing a co-expression plasmid containing both the 806.077 HuVK4 light chain and the 806.077 HuVH1 heavy chain variable region antibody genes. In this case, the plasmid the pNG3-Vkss-806.077HuVK4-HuCK-Neo vector, which contains the humanised light chain variable region HuVK1 (SEQ ID NOS: 70 and 71) was digested using the restriction enzymes BamHI and SalI and the vector run on an 1% agarose gel and the vector band purified. The plasmid pNG4-VHss-806.077HuVH1-HuIgG2 CH1' (which contains the humanised 806.077 HuVH1 heavy chain variable region (SEQ ID NOS: 56 and 57) was digested using the restriction enzymes BglII and SalI, the reaction run on an 2% agarose and the fragment band excised and purified. The DNA fragment recovered was ligated into the prepared pNG3-Vkss-806.077HuVK4-HuCK-Neo vector to produce clones of the desired HuVH1/ HuVK4 co-expression vector.

As described in Example 11, these constructs were transfected into NS0 myeloma cells (ECACC No. 85110503) via standard techniques of electroporation and transfectants selected for the property of G418 resistance. The clones obtained were tested for both

antibody expression in anti-human antibody Fd ELISA and CEA binding ELISA assays. Clones found to show the best expression and CEA binding levels were selected, expanded and product expressed. Human $F(ab')_2$ antibody fragment was then purified from the culture supernatant as described in Example 102.

Example 39-47

Expression of humanised $F(ab')_2$ fragments with various classes of human heavy chain constant regions

Other classes of chimaeric heavy chain Fd constructs may be used. Accordingly, additional variants of the heavy chain vectors have been made which contain either HuIgG1CH1' (SEQ ID NOS: 20 and 21) or HuIgG3CH1' (SEQ ID NOS: 24 and 115), the constant regions of which are substituted for the HuIgG2CH1' gene (SEQ ID NOS: 22 and 23). The vectors created were pNG4-VHss-HuIgG1 CH1' and pNG4-VHss-HuIgG3 CH1' respectively. The heavy chain antibody variable region in question can be excised from the appropriate pNG4-VHss-"VH variable region"-HuIgG2 CH1' plasmid by digestion with EcoRI and SacI restriction enzymes and cloned into the similarly restricted pNG4-VHss-HuIgG1CH1' or pNG4-VHss-HuIgG3 CH1' vector and thus produce a completed heavy chain Fd sequence. As described above, once the individual heavy and light chain sequences are constructed, a heavy chain Fd gene expression cassette (including both promoter and gene can be excised by restriction digestion and the fragment cloned between into the appropriate sites of the light chain vector to produce the final co-expression vector. The table below describes Examples 39-47 in which various heavy and light chain variable regions have been combined with a number of different classes of human heavy chain constant regions.

In Example 44, the vector pNG4-VHss-HuIgG3 CH1' was digested with the restriction enzymes EcoRI and SacI restriction enzymes and the vector fragment isolated as previously described. The HuVH1 heavy chain antibody variable region (SEQ ID NOS: 54 and 55) was excised from the pNG4-VHss-806.077HuVH1-HuIgG2 CH1' plasmid by digestion with EcoRI and SacI restriction enzymes and the fragment cloned into the similarly restricted pNG4-VHss-HuIgG3 CH1' vector to produce a completed humanised IgG3 heavy chain Fd sequence (SEQ ID NOS: 94 and 95) in the completed vector pNG4-VHss-806.077HuVH1-HuIgG3 CH1'. The heavy chain Fd gene expression cassette (including both promoter and gene) was excised as a BglII/SalI fragment and cloned into the BamHI/SalI

sites of the light chain vector pNG3-Vkss-806.077HuVK1-HuCK-Neo (containing the HuVK1-HuCK humanised light chain SEQ ID NOS: 51 and 52) which had been digested using the restriction enzymes BamHI and SalI , run on an 1% agarose, the vector band purified. This produced a co-expression vector (pNG 806HuVH1/HuVK3/HuIgG3) from which the humanised 806.077HuVH1/HuVK1-HuIgG3/Kappa.Fd antibody fragment could be expressed.

Table

Example No.	Humanised heavy chain	SEQ ID NOS	Humanised light chain	SEQ ID NOS	Co-expression Plasmid Vector
39	HuVH1-HuIgG1	92 and 93	HuVK1-HuCK	51 and 52	Png 806HuVH1/HuVK1/HuIgG1
40	HuVH1-HuIgG2	56 and 57	HuVK1-HuCK	51 and 52	pNG 806HuVH1/HuVK1/HuIgG2
41	HuVH1-HuIgG3	94 and 95	HuVK1-HuCK	51 and 52	pNG 806HuVH1/HuVK1/HuIgG3
42	HuVH1-HuIgG1	92 and 93	HuVK3-HuCK	96 and 97	pNG 806HuVH1/HuVK3/HuIgG1
43	HuVH1-HuIgG2	56 and 57	HuVK3-HuCK	96 and 97	pNG 806HuVH1/HuVK3/HuIgG2
44	HuVH1-HuIgG3	94 and 95	HuVK3-HuCK	96 and 97	pNG 806HuVH1/HuVK3/HuIgG3
45	HuVH1-HuIgG1	92 and 93	HuVK4-HuCK	98 and 99	pNG 806HuVH1/HuVK4/HuIgG1
46	HuVH1-HuIgG2	56 and 57	HuVK4-HuCK	98 and 99	pNG 806HuVH1/HuVK4/HuIgG2
47	HuVH1-HuIgG3	94 and 95	HuVK4-HuCK	98 and 99	pNG 806HuVH1/HuVK4/HuIgG3

In Example 47, the vector pNG4-VHss-HuIgG3 CH1' was digested with EcoRI and SacI restriction enzymes and the vector fragment isolated. The HuVH1 heavy chain antibody variable region (SEQ ID NOS: 54 and 55) was excised from the pNG4-VHss-HuVH1-HuIgG2 CH1' plasmid by digestion with EcoRI and SacI restriction enzymes and the

fragment cloned into the similarly restricted pNG4-VHss-HuIgG3 CH1' vector. This produces a completed humanised IgG3 heavy chain Fd sequence (SEQ ID NOS: 94 and 95) in the completed vector pNG4-VHss-806.077HuVH1-HuIgG3 CH1'. The heavy chain Fd gene expression cassette (including both promoter and gene) was excised as a BglII/SalI fragment and cloned into the BamHI/SalI sites of the light chain vector pNG3-Vkss-806.077HuVK4-HuCK-Neo vector, (containing HuVK4-HuCK humanised light chain SEQ ID NOS: 98 and 99) which had been digested using the restriction enzymes BamHI and SalI, run on an 1% agarose, the vector band purified. This produced a co-expression vector construct pNG 806HuVH1/HuVK4/HuIgG3 from which the humanised HuVH1/HuVK1-HuIgG3/Kappa.Fd antibody fragment could be expressed.

The other Examples shown in the table above were all produced in a similar manner to that described in the Examples 44 and 47. However, in the case of the constructs containing human IgG1, the final co-expression vector construction was made by cloning the heavy chain Fd gene expression cassette (including both promoter and gene) excised as a BglII/BamHI fragment (because there is an internal SalI restriction site in the HuIgG1 CH1' constant region gene) and cloned into the BamHI site of the appropriately prepared light chain vector. In this case the orientation of the heavy chain cassette must be checked. This was achieved by restriction digestion (e.g. with the restriction enzyme Hind III) and agarose gel electrophoresis analysis in which the resulting fragment sizes were viewed relative to comparable fragments from a similarly digested HuIgG2 version (Examples 11-38). When the fragmentation patterns matched for both constructs we could be sure that the heavy chain cassette was in the correct orientation.

As previously described in Example 11, these constructs were transfected into NS0 myeloma cells (ECACC No. 85110503) via standard techniques of electroporation and transfectants selected for the property of G418 resistance. The clones obtained were tested for both antibody expression in the anti-human antibody Fd ELISA and CEA binding ELISA assays and the clones found to show the best expression and CEA binding levels were selected, expanded and grown for gene expression. As before, the human $F(ab')_2$ antibody fragment was then purified from the culture supernatant as described in Example 102.

Example 48

Preparation of humanised 806.077 F(ab')$_2$-[A248S,G251T,D253K]HCPB fusion protein

This Example describes the preparation of a gene encoding a humanised Fd heavy chain fragment of 806.077 linked to [A248S,G251T,D253K]HCPB and its co-expression with a gene encoding a humanised light chain of 806.077 and a gene encoding the pro domain of human carboxypeptidase B to give the F(ab')$_2$ protein with a molecule of [A248S,G251T,D253K]HCPB at the C-terminus of each of the heavy chain fragments. The constant and hinge regions of of the humanised Fd heavy chain fragment are derived from the human IgG3 antibody isotype. The expressed protein is also referred to as antibody-enzyme fusion protein.

(a) Preparation of a gene encoding humanised Fd heavy chain fragment of 806.077 linked to [A248S,G251T,D253K]HCPB and its cloning into pEE6

A gene encoding humanised 806.077 Fd linked to [A248S,G251T,D253K]HCPB was generated by PCR from pZEN1921 (Reference Example 2). A first PCR was set up with template pZEN1921 (2ng) and oligonucleotides SEQ ID NO: 100 and SEQ ID NO: 101 (100pM of each) in buffer (100µl) containing 10mM Tris-HCl (pH8.3), 50mM KCL, 1.5mM $MgCl_2$, 0.125mM each of dATP, dCTP, dGTP and dTTP. The reaction was incubated at 94^{o}C for 5 min then thermostable DNA polymerase (2.5u, 0.5 µl) was added and the mixture overlaid with mineral oil (100µl) and the reaction mixture incubated at 94^{o}C for 1 min, 53^{o}C for 1 min and 72^{o}C for 2.5 min for 25 cycles, plus 10 min at 72^{o}C. The PCR product of 536 base pairs was isolated by electrophoresis on a 1% agarose (Agarose type I, Sigma A-6013) gel followed by excision of the band from the gel and isolation of the DNA fragment.

A second PCR was set up with template IgG3-pBSIIKS+ (8.7ng, described in Reference Example 4) and oligonucleotides SEQ ID NO: 102 and SEQ ID NO: 103 and the 954 base pairs fragment isolated as described above. The products from the 2 PCRs were combined (either at 0.2, 1.0 or 5.0 ng/µl) in PCR buffer as described above. The mixture was incubated for at 94^{o}C for 5 min then 10 cycles at 94^{o}C for 1 min and 63^{o}C for 4 min. Oligos SEQ ID NOS: 101 and 102 (100pM of each) in PCR buffer (50µl) were added. After incubation at 94^{o}C for 3 min, the mixture was further incubated at 94^{o}C for 1.5 min, 53^{o}C for 2 min and 72^{o}C for 2 min for 25 cycles plus 10 min at 72^{o}C. In this process, the G base at position 508 in SEQ ID NO: 115 was changed to an A base.

The PCR product of 1434 base pairs was isolated by electrophoresis on a 1% agarose gel, purified and digested with NheI (20u) and XbaI (80u) (New England Biolabs Inc.,) in a total volume of 100µl containing 10mM Tris HCl (pH7.9), 50mM NaCl, 10mM $MgCl_2$, 1mM DTT and BSA (100µg/ml) for 4h at 37°C. The resulting fragment was again isolated by electrophoresis on a 1% agarose gel and purified. In a similar digestion, vector pNG4-VHss-806.077huVH1-HuIgG2CH1' (10µg; Example 11) was cut with NheI and XbaI then calf intestinal alkaline phosphatase (1µl; New England Biolabs, 10u/µl) was added to the digested plasmid to remove 5' phosphate groups and incubation continued at 37°C for a further 30 minutes. Phosphatase activity was destroyed by incubation at 70°C for 10 minutes. The NheI-XbaI cut plasmid was purified from an agarose gel. The NheI-XbaI digested PCR product from above (about 500ng) was ligated with the above cut plasmid DNA (about 200ng) in 20µl of a solution containing 50mM Tris-Hcl (pH7.8), 10mM $MgCl_2$, 10mM DTT, 1mM ATP, 50 µg/ml BSA and 400u T4 DNA ligase (New England Biolabs, Inc) at 25°C for 4h. A 1µl aliquot of the reaction was used to transform 20µl of competent E. coli DH5α cells. Transformed cells were plated onto L-agar plus 100µg/ml ampicillin. Potential clones containing the gene for humanised 806.077 Fd-[A248S,G251T,D253K]HCPB were identified by PCR. Each clone was subjected to PCR as described above with oligonucleotides SEQ ID NOS: 104 and 105. A sample (10µl) of the PCR reaction was analysed by electrophoresis on a 1% agarose gel. Clones containing the required gene were identified by the presence of a 512 base pairs PCR product. Clones producing the 512 base pairs band were used for DNA minipreps. The DNA samples were checked by digestion with HindIII and XbaI for the presence of 3751 base pairs and 1862 base pairs fragments. Clones containing these fragments on digestion of the DNA with HindIII and XbaI were used for large scale plasmid DNA preparation and the sequence of the insert confirmed by DNA sequence analysis. The sequence of the expected insert is shown in SEQ ID NO: 112 Of the clones examined above, 2 contained the expected sequence but with a single base mutation. Clone 54 (also designated pMF195) had an T base at position 605 in SEQ ID NO: 112 in place of the A base, whereas clone 68 (also designated pMF198) had a C base at position 1825 instead of the expected T base. The sequence shown in SEQ ID NO: 112 was prepared from pMF195 and and pMF198 by digesting both (10 µg of each) with XmaI (10u) and XbaI (100u) (New England Biolabs) in buffer (100µl) containing 20mM Tris acetate (pH7.9) 50mM potassium acetate. 10mM Mg acetate. 1mM DTT and BSA (100µg/ml). The 215 base pairs fragment from pMF195 and the

vector fragment from pMF198 (following treatment with alkaline phosphatase) were isolated from a 1% agarose gel and ligated together as described previously. The ligation mix was used to transform competent DH5α cells. The transformed cells were plated onto L agar plus ampicillin and resulting colonies screened by digestion of the DNA with XmaI and XbaI for the presence of 5400 base pairs and 215 base pairs fragments. Positive clones were used for large scale plasmid DNA preparation and the sequence of the insert confirmed by DNA sequence analysis. The plasmid containing the 806.077 Fd-[A248S,G251T,D253K]HCPB gene from clone number 102 was named pMF213. The HindIII-XbaI fragment from pMF213 was cloned into pEE6 [this is a derivative of pEE6.hCMV - Stephens and Cockett (1989) Nucleic Acids Research 17, 7110 - in which a HindIII site upstream of the hCMV promoter has been converted to a BglII site] in DH5α (screened by PCR with oligonucleotides SEQ ID NOS: 106 and 107 for a 2228 base pairs insert) to give pMF221.

(b) Preparation of a co-expression vector for expression of antibody-enzyme fusion protein

To generate vectors capable of expressing the antibody-enzyme fusion protein in eukaryotic cells, the GS-System™ (Celltech Biologics) was used (WO 87/04462, WO 89/01036, WO 86/05807 and WO 89/10404). The procedure requires cloning the humanised antibody light chain gene into the HindIII-XmaI region of vector pEE14. This vector is described by Bebbington in METHODS: A Companion to methods in Enzymology (1991) 2, 136-145. To construct the expression vector, plasmids pEE14 and pNG3-VKss-806.077HuVK4-HuCK-Neo (Example 14) were digested with HinIII and XmaI as described above. The appropriate vector (from pEE14) and insert (732 base pairs from pNG3-VKss-806.077HuVK4-HuCK-Neo) from each digest were isolated from a 1% agarose gel and ligated together and used to transform competent DH5α cells. The transformed cells were were plated onto L agar plus ampicillin (100μg/ml). Colonies were screened by restriction analysis of isloated DNA for the presence of a 732 base pairs fragment on digestion of the DNA with HindIII and XmaI. Clones producing a 732 base pairs restriction fragment were used for large scale plasmid DNA preparation and the sequence of the insert confirmed by DNA sequence analysis. The plasmid containing the humanised light chain sequence of SEQ ID NO: 70 in pEE14 was named pEE14-806.077HuVK4-HuCK.

To make the co-expression vector, pMF221 (10μg) was cut with BglII (20u) and SalI (40U) in buffer (100μl) containing 10mM Tris-HCl (pH 7.9), 150mM NaCl, 10mM

$MgCl_2$, 1mM DTT and BSA (100μg/ml) and the 4560 base pairs fragment isolated by agarose gel electrophoresis and purified. Similarly, pEE14-806.077HuVK4-HuCK was cut with BamHI (40u) and SalI (40u) and the 9.95kb vector fragment isolated and ligated to the BglII-SalI fragment from pMF221 and cloned into DH5α. Colonies were screened by PCR with 2 sets of oligonucleotides (SEQ ID NOS: 104 and 105, and SEQ ID NOS: 108 and 109). Clones giving PCR products of 185 base pairs and 525 base pairs respectively were characterised by DNA sequencing. A clone with the correct sequence was named pMF228 - light chain/Fd-mutant HCPB co-expression vector in DH5α. The humanised Fd-mutant HCPB sequence is shown in SEQ ID NO: 113. Residues 1 to 19 are the signal sequence, residues 20 to 242 are the humanised variable and IgG3 CH1 region, residues 243 to 306 are the IgG3 hinge region and residues 307 to 613 are the mutant HCPB sequence with the changes at residues 248, 251 and 253 from the human HCPB sequence. The changes in the HCPB sequence occur in SEQ ID NO: 113 at postions 554 (Ser), 557 (Thr) and 559 (Lys) respectively.

(c) Preparation of a vector for expression of the pro domain of proHCPB

A second eukaryotic expression plasmid, pEE12 containing a gene for the prepro sequence, for secretion of the pro domain with an additional C-terminal leucine residue (termed pro-L), of preproHCPB was prepared as described in Reference Example 17 of International Patent Application Number WO 96/20011. Plasmid pMF161 was prepared by PCR from pMF18 as described for the unmodified prepro sequence, but using oligonucleotides SEQ ID NOS: 110 and 111. The 359 base pairs fragment was cloned into pBluescript to give pMF141 and subsequently into pEE12 to give pMF161. The protein sequence of pro-L is shown in SEQ ID NO: 114.

(d) Expression of antibody-enzyme fusion protein in eukaryotic cells

For expression in eukaryotic cells, vectors containing genes capable of expressing the antibody enzyme-fusion protein (pMF228) and the pro-L sequence (pMF161) were co-transfected into COS-7 cells. COS cells are an African green monkey kidney cell line, CV-1, transformed with an origin-defective SV40 virus and have been widely used for short-term transient expression of a variety of proteins because of their capacity to replicate circular plasmids containing an SV40 origin of replication to very high copy number. There are two widely available COS cell clones, COS-1 and COS-7. The basic

methodology for transfection of COS cells is described by Bebbington in Methods: A Companion to Methods in Enzymology (1991) 2, p. 141. For expression of HCPB, the plasmid vectors pMF48 and pMF67 (2μg of each) were used to transfect the COS-7 cells (2×10^5) in a six-well culture plate in 2ml Dulbecco's Modified Eagle's Medium (DMEM) containing 10% heat inactivated foetal calf serum (FCS) by a method known as lipofection - cationic lipid-mediated delivery of polynucleotides [Felgner et al. in Methods: A Companion to Methods in Enzymology (1993) 5, 67-75]. The cells were incubated at 37°C in a CO_2 incubator for 20h. The mix of plasmid DNA in serum-free medium (200μl) was mixed gently with LIPOFECTIN™ reagent (12μl) and incubated at ambient temperature for 15min. The cells were washed with serum-free medium (2ml). Serum-free medium (600μl) was added to the DNA/LIPOFECTIN™ and the mix overlaid onto the cells which were incubated at 37°C for 6h in a CO_2 incubator. The DNA containing medium was replaced with normal DMEM containing 10% FCS and the cells incubated as before for 72h. Cell supernatants (diluted 1:10 with 0.025M Tris-HCl pH7.5; 125μl) were analysed for activity against Hipp-Glu (5h assay, in a total volume of 250μl) essentially as described in Example 103. The diluted supernatant resulted in 18.4% hydrolysis of the Hipp-Glu substrate.

Alternatively, the unmodified pro domain (from plasmid pMF67 described in Reference Example 17 of International Patent Application Number WO 96/20011) can be used in place of the pro-L expression plasmid in the above experiment.

Large scale expression of proteins from COS cells is described by Ridder et al. (1995) in GENE 166, 273-276 and by Blasey et al. (1996) in CRYOTECHNOLOGY 18, 183-192.

For stable expression in CHO cells, the procedures described by Bebbington in METHODS: A Companion to Methods in Enzymology (1991) 2, 136-145 using GS selection with 25μM and 50μM MSX are followed. Alternatively, lipofection, essentially as described above for transfection of COS cells may also be used to transfect CHO cells. The cells are transfected with a mixture of plasmids pMF228 and pMF161 or pMF228 and pMF67. Supernatants from surviving colonies are screened by CEA ELISA (described in Example 11) and Western analysis (described below) for the presence of a 170kDa band corresponding to the required antibody enzyme fusion protein. Supernatants, suitably diluted, are also screened for enzyme activity as described in Example 103. Colonies

expressing the desired antibody enzyme fusion protein are cultured at the required scale (see for Example the publication by M E Reff (1993) in Current Opinion in Biotechnology 4, 573-576 and references cited therein) and fusion protein purified from cell culture supernatant by one or more of the methods described in Example 102.

(e) Western analysis

Western blot analysis was performed as described as follows. Aliquots (20µl) of each supernatant sample were mixed with an equal volume of sample buffer (62.5mM Tris, pH6.8, 1% SDS, 10% sucrose and 0.05% bromophenol blue) with and without reductant. The samples were incubated at 65°C for 10 minutes before electrophoresis on a 8-18% acrylamide gradient gel (EXCEL™ gel system from Pharmacia Biotechnology Products) in a MULTIPHOR™ II apparatus (LKB Produkter AB) according to the manufacturer's instructions. After electrophoresis, the separated proteins were transfered to a membrane (HYBOND™ C-Super,Amersham International) using a NOVABLOT™ apparatus (LKB Produkter AB) according to protocols provided by the manufacturer. After blotting, the membrane was air dried.

The presence of antibody fragments was detected by the use of an anti-human kappa antibody (Sigma A7164, goat anti-human Kappa light chain peroxidase conjugate) used at 1:2500 dilution. The presence of human antibody fragments was visualised using a chemiluminescence system (ECL™ detection system, Amersham International).

Examples 49-74

Preparation of other humanised 806.077 F(ab')$_2$-mutant HCPB fusion proteins

These Examples describe preparation of genes encoding humanised Fd heavy chain fragments of 806.077 linked to a mutant HCPB (D253K; G251T,D253K; A248S,G251T,D253K) and their co-expression with a gene encoding a humanised light chain of 806.077 and a gene encoding the pro domain of human carboxypeptidase B to give the F(ab')$_2$ protein with a molecule of mutant HCPB at the C-terminus of each of the heavy chain fragments. The constant and hinge regions of of the humanised Fd heavy chain fragment are derived from the human IgG1 or IgG2 or IgG3 antibody isotype. The expressed proteins are also referred to as antibody-enzyme fusion proteins.

The procedures described in Example 48 are repeated with the appropriate sequences derived from the table shown below. Oligonucleotides for PCR constructions and clone screening are readily derived from the appropriate sequences.

To change the mutant HCPB sequence, the PCR template, plasmid pZEN1921, in part (a) of Example 48 is replaced with pZEN1860 for [G251T,D253K]HCPB (described in Reference Example 1) or pICI1713 for [D253K]HCPB (described in International Patent Application Number WO 96/20011).

To change the antibody heavy chain constant and hinge region, the PCR template, vector IgG3-pBSIIKS+, in part (a) of Example 48 is replaced with pNG4-VHss-HuIgG1CH1' (described in Examples 39-47) or pNG4-VHss-HuIgG2CH1' (NCIMB No. 40797).

To change the humanised antibody light chain sequence, the vector pEE14-806.077HuVK4-HuCK in part (b) of Example 48 is replaced with pEE14-806.077HuVK1-HuCK or pEE14-806.077HuVK3-HuCK. The vectors pEE14-806.077HuVK1-HuCK and pEE14-806.077HuVK3-HuCK are prepared as described for pEE14-806.077HuVK4-HuCK in part (b) of Example 48 but using the 732 base pairs HindIII-XmaI fragment from pNG-VHss-806.077HuVK1-Neo and pNG-VHss-806.077HuVK3-Neo respectively (described in Examples 12-38) in place of the HindIII-XmaI fragment from pNG-VHss-806.077HuVK4-Neo.

Antibody-enzyme fusion protein variants for each Example are shown in the table below.

Table

Example No.	Humanised Heavy chain	Humanised Light chain	Mutant HCPB Enzyme
49	HuVH1-HuIgG3	HuVK4-HuCK	[D253K]HCPB
50	HuVH1-HuIgG3	HuVK4-HuCK	[G251T,D253K]HCPB
51	HuVH1-HuIgG3	HuVK1-HuCK	[A248S,G251T,D253K]HCPB
52	HuVH1-HuIgG3	HuVK1-HuCK	[D253K]HCPB
53	HuVH1-HuIgG3	HuVK1-HuCK	[G251T,D253K]HCPB
54	HuVH1-HuIgG3	HuVK3-HuCK	[A248S,G251T,D253K]HCPB
55	HuVH1-HuIgG3	HuVK3-HuCK	[D253K]HCPB
56	HuVH1-HuIgG3	HuVK3-HuCK	[G251T,D253K]HCPB
57	HuVH1-HuIgG1	HuVK4-HuCK	[A248S,G251T,D253K]HCPB

58	HuVH1-HulgG1	HuVK4-HuCK	[D253K]HCPB
59	HuVH1-HulgG1	HuVK4-HuCK	[G251T,D253K]HCPB
60	HuVH1-HulgG1	HuVK1-HuCK	[A248S,G251T,D253K]HCPB
61	HuVH1-HulgG1	HuVK1-HuCK	[D253K]HCPB
62	HuVH1-HulgG1	HuVK1-HuCK	[G251T,D253K]HCPB
63	HuVH1-HulgG1	HuVK3-HuCK	[A248S,G251T,D253K]HCPB
64	HuVH1-HulgG1	HuVK3-HuCK	[D253K]HCPB
65	HuVH1-HulgG1	HuVK3-HuCK	[G251T,D253K]HCPB
66	HuVH1-HulgG2	HuVK4-HuCK	[A248S,G251T,D253K]HCPB
67	HuVH1-HulgG2	HuVK4-HuCK	[D253K]HCPB
68	HuVH1-HulgG2	HuVK4-HuCK	[G251T,D253K]HCPB
69	HuVH1-HulgG2	HuVK1-HuCK	[A248S,G251T,D253K]HCPB
70	HuVH1-HulgG2	HuVK1-HuCK	[D253K]HCPB
71	HuVH1-HulgG2	HuVK1-HuCK	[G251T,D253K]HCPB
72	HuVH1-HulgG2	HuVK3-HuCK	[A248S,G251T,D253K]HCPB
73	HuVH1-HulgG2	HuVK3-HuCK	[D253K]HCPB
74	HuVH1-HulgG2	HuVK3-HuCK	[G251T,D253K]HCPB

Example 75

Preparation of [A248S,G251T,D253K]HCPB-(humanised 806.077)F(ab')$_2$ fusion protein

This Example describes the preparation of a gene encoding pro-[A248S,G251T,D253K]HCPB linked to a humanised (version 1 VH with Human IgG3) Fd heavy fragment of antibody 806.077, and its co-expression with a gene encoding a humanised light chain (version 4 VK with CK) of the 806.077 antibody. This gives the F(ab')$_2$ protein with a molecule of the pro-[A248S,G251T,D253K]HCPB at the N-terminus of each of the heavy chain fragments. The enzyme is activated by the enzymatic removal of the pro domain using trypsin.

Standard molecular biology techniques, such as restriction enzyme digestion, ligation, kinase reactions, dephosphorylation, polymerase chain reaction (PCR), bacterial transformations, gel electrophoresis, buffer preparation and DNA generation, purification and isolation, were carried out as described by Maniatis et al., (1989) Molecular Cloning, A Laboratory Manual; Second edition: Cold Spring Harbor Laboratory, Cold Spring Harbor,

New York, or following the recommended procedures of manufacturers of specific products. In most cases enzymes were purchased from New England BioLabs, but other suppliers, and equivalent procedures may be used. Oligonucleotide sequences were prepared in an Applied Biosystems 380A DNA synthesiser from 5'dimethoxytrityl base-protected nucleoside-2-cyanoethyl-N,N'-di-isopropyl-phosphoramidites and protected nucleoside linked to controlled-pore glass supports on a 0.2 μmol scale, according to the protocols supplied by Applied Biosystems Inc.

Mutants of HCPB, native HCPB and HCPB fusion proteins were assayed for their ability to convert hippuryl-L-glutamic acid or hippuryl-L-arginine acid to hippuric acid using an HPLC based assay as described in Example 103 or International Patent Application Number WO 96/20011 Example 20.

Immunoassay techniques were carried out using methods based on those described by Tijssen, (1985) Practice and Theory of Enzyme Immunoassays, Laboratory Techniques in Biochemistry and Molecular Biology Volume 15, Elsevier Science Publishers, Amsterdam, or following the recommended procedures of manufacturers of specific products.

To generate plasmids capable of expressing the antibody-enzyme fusion protein in eukaryotic cells the GS-System (Celltech Biologics) was used (details in International Patent Application Numbers WO 87/04462, WO 89/01036, WO 86/05807 and WO 89/10404) with the two plasmids pEE6 (a derivative of pEE6.hCMV in which the HindIII restriction site upstream of the hCMV promoter has been converted to a BglII site {Stephens and Cockett, 1989, Nucleic Acids Research, 17, 7110}) and pEE12 (a derivative of pSV2.GS with a number of restriction sites removed {Bebbington et al, 1992, Bio/Technology, 10. 169}).

a) Cloning pre-pro-HCPB up to restriction enzyme XmaI cut site (position 1048 in SEQ ID NO: 124)

Double stranded DNA of plasmid pMF18 (as described in International Patent application Number WO 96/20011 Reference Example 19), a construct consisting of pre-pro-HCPB cloned into vector pBluescript II KS+ (Stratagene), was prepared using standard DNA technology (Qiagen plasmid kit or similar), and restriction digested with HindIII and XmaI enzymes, being very careful to ensure complete digestion. Restriction enzyme HindIII cuts the pMF18 plasmid just prior to the start of the pre-sequence of the HCPB gene. and XmaI cuts at the codon for amino acid 240 (proline) of the mature protein, the HindIII to XmaI

DNA piece is referred to as the pre-pro-HCPB fragment. DNA of the correct size, containing the pre-pro-HCPB fragment (about 1061 base pairs) was purified.

Double stranded DNA of plasmid vector pUC19 (New England BioLabs) was prepared, restriction digested with HindIII and XmaI, and purified (about 2651 base pairs) in a similar manner to the pre-pro-HCPB fragment. Ligation mixes were prepared to clone the HCPB gene fragment into the pUC19 vector, using a molar ratio of about 1 vector to 2.5 insert, and a final DNA concentration of about 2.5ng/µl, in the presence of T4 DNA ligase, 1mM ATP and enzyme buffer. Following the ligation reaction the DNA mixture was used to transform E.coli strain DH5α. Cell aliquots were plated on L-agar nutrient media containing 100µg/ml ampicillin as selection for plasmid vector, and incubated overnight at 37°C. A number of colonies were picked and used for mini-preparations of double stranded plasmid DNA. These DNA samples were analysed by restriction enzyme digestion, and a construct of the correct configuration identified. This plasmid containing the pre-pro-HCPB fragment up to the XmaI site in the mature gene is known as pCF003.

b) Cloning [A248S,G251T,D253K]HCPB from position G241 + linker and 5 amino acids of VH

To separate the HCPB from the Fd sequence a neutral peptide linker consisting of (Glycine-Glycine-Glycine-Serine)$_3$ was introduced into the sequence during the PCR. In order to generate the fragment of the mutant [A248S,G251T,D253K]HCPB sequence (as documented in Reference Example 2) and add the peptide linker and the first 5 amino acids of the humanised 806.077 VH, a PCR was set up using 100pMols of primers CME 00971 and CME 00972 (SEQ ID NOs: 122 and 123) in the presence of approximately 5ng of pZen1921 DNA, dNTPs to a final concentration of 200µM, Taq polymerase reaction buffer, and 2.5U of Taq polymerase in a final volume of 100µl. The mixture was heated at 94°C for 10 minutes prior to addition to the Taq enzyme, and the PCR incubation was carried out using 30 cycles of 94°C for 1.5 minutes, 55°C for 2 minutes, and 72°C for 2 minutes, followed by a single incubation of 72°C for 10 minutes at the end of the reaction. The PCR product containing the [A248S,G251T,D253K]HCPB fragment (about 298 base pairs) was analysed for DNA of the correct size by agarose gel electrophoresis and found to contain predominantly a band of the correct size. The remainder of the product from the reaction mix was purified and separated from excess reagents using a microconcentrator column (Centricon™ 100, Amicon), followed by DNA isolation by ethanol/sodium acetate precipitation, centrifugation, vacuum drying and

re-suspension in distilled water. The isolated DNA was restriction digested with enzymes XmaI and EcoRI, and a band of the correct size (about 271 base pairs) purified.

Double stranded DNA of plasmid pCF003 (described above) prepared using standard DNA technology (Qiagen plasmid kits or similar), was restriction digested with XmaI and EcoRI enzymes, and a band of the correct size (about 2696 base pairs) purified.

Ligation mixes were prepared to clone the mutant HCPB gene fragment into the vector, using a molar ratio of about 1 vector to 2.5 insert (1 pCF003 to 2.5 [A248S,G251T,D253K]HCPB fragment PCR product), and a final DNA concentration of about 2.5ng/µl, in the presence of T4 DNA ligase, 1mM ATP and enzyme buffer. Following the ligation reaction the DNA mixture was used to transform E.coli strain DH5α. Cell aliquots were plated on L-agar nutrient media containing 100µg/ml ampicillin as selection for plasmid vector, and incubated overnight at 37°C. About 200 colonies were picked and plated onto duplicate sterile nitro-cellulose filters (Schleicher and Schull), pre-wet on plates of L-agar nutrient media containing 100µg/ml ampicillin as selection for plasmid vector, and incubated overnight at 37°C. One duplicate plate was stored at 4°C, and acted as a source of live cells for the colonies, the other plate was treated to denature and fix the DNA from the individual colonies to the nitro-cellulose. The nitro-cellulose filter was removed from the agar plate and placed in succession onto filter papers (Whatman) soaked in: 1. 10% SDS for 2 minutes; 2. 0.5M NaOH, 1.5M NaCl for 7 minutes; 3. 0.5M NaOH, 1.5M NaCl for 4 minutes; 4. 0.5M NaOH, 1.5M NaCl for 2 minutes; 5. 0.5M Tris pH7.4, 1.5M NaCl for 2 minutes; and 6. 2xSSC (standard saline citrate) for 2 minutes. The filter was then placed on a filter paper (Whatman) soaked in 10xSSC and the denatured DNA was crossed linked to the nitro-cellulose by ultra violet light treatment (Spectrolinker XL-1500 UV crosslinker). The filters were allowed to air dry at room temperature, and were then pre-hybridised at 60°C for one hour in a solution of 6xSSC with gentle agitation (for example using a Techne HB-1D hybridizer). Note pre-hybridisation blocks non-specific DNA binding sites on the filters.

In order to determine which colonies contain DNA inserts of interest the DNA cross-linked to the nitro-cellulose filter was hybridised with a radio-labelled ^{32}P-DNA probe prepared from the [A248S,G251T,D253K]HCPB purified PCR DNA fragment (see above). About 50ng of DNA was labelled with 50µCi of ^{32}P-dCTP (>3000Ci/mMol) using T7 DNA polymerase in a total volume of 50µl (Pharmacia T7 Quickprime kit), and the reaction allowed to proceed for 15 minutes at 37°C. The labelled probe was heated to 95°C for 2

minutes. to denature the double stranded DNA, immediately added to 10ml of 6xSSC at 60°C, and this solution was used to replace the pre-hybridisation solution on the filters. Incubation with gentle agitation was continued for about 3 hours at 60°C. After this time the hybridisation solution was drained off, and the filters were washed twice at 60°C in 2xSSC for 15 minutes each time. Filters were then gently blotted dry, covered with cling film (Saran™ wrap or similar), and exposed against X-ray film (for example Kodak X-OMAT-ARS™) overnight at room temperature. Following development of the film, colonies containing inserts of interest were identified as those which gave the strongest exposure (darkest spots) on the X-ray film. In this series of experiments about 15% of the colonies gave positive hybridisation. From this 12 colonies were chosen for further screening. These colonies were picked from the duplicate filter, streaked and maintained on L-agar nutrient media containing 100µg/ml ampicillin, and grown in L-broth nutrient media containing 100µg/ml ampicillin.

The selected colonies were used for mini-preparations of double stranded plasmid DNA. These DNA samples were analysed by restriction enzyme digestion, and constructs of the correct configuration identified. In order to ensure that no changes to the DNA sequence had been introduced during the PCR a number of clones with correct restriction mapping were taken for DNA preparation using standard technology (Qiagen plasmid kits or similar), and the inserts sequenced using several separate oligonucleotide primers. A construct of the correct sequence was identified, and this plasmid containing the pre-pro-[A248S,G251T,D253K]HCPB-linker-humanised 806.077 VH gene up to the PstI site (at amino acid 5)(position 1301 in SEQ ID NO: 124) is termed pCF004.

c. Cloning Humanised 806.077 Fd

Double stranded DNA of plasmid pNG4-VHss-HuVH1-806.077-IgG3CH1', a construct consisting of the humanised 806.077 version 1 VH with human IgG3 CH1 and hinge region cloned into vector pNG4 (see Example 44), was prepared using standard DNA technology (Qiagen plasmid kit or similar), and restriction digested with PstI and XmaI enzymes. DNA of the correct size, containing the humanised 806.077 Fd fragment (about 854 base pairs) was purified. Double stranded DNA of plasmid vector pUC19 (New England BioLabs) was prepared, restriction digested with PstI and XmaI, and purified (about 2659 base pairs) in a similar manner to the humanised 806.077 Fd fragment.

Aliquots of both restricted and purified DNA samples were checked for purity and concentration estimation using agarose gel electrophoresis compared with known standards.

From these estimates ligation mixes were prepared to clone the humanised 806.077 Fd gene fragment into the pUC19 vector, using a molar ratio of about 1 vector to 2.5 insert, and a final DNA concentration of about 2.5ng/μl, in the presence of T4 DNA ligase, 1mM ATP and enzyme buffer.

Following the ligation reaction the DNA mixture was used to transform E.coli strain DH5α. Cell aliquots were plated on L-agar nutrient media containing 100μg/ml ampicillin as selection for plasmid vector, and incubated overnight at 37°C. A number of colonies were picked and used for mini-preparations of double stranded plasmid DNA. These DNA samples were analysed by restriction enzyme digestion, and a construct of the correct configuration identified. This plasmid containing the humanised 806.077 Fd fragment from the PstI site to the XmaI site is known as pCF005.

d) Cloning humanised 806.077 Fd into pre-pro-[A248S,G251T,D253K]HCPB-linker construct

Double stranded DNA of plasmid pCF005 (as documented above), was prepared using standard DNA technology (Qiagen plasmid kit or similar), and restriction digested with PstI and EcoRI enzymes. DNA of the correct size, containing the humanised 806.077 Fd fragment (about 870 base pairs) was purified. Double stranded DNA of plasmid vector pCF004 (as documented above) was prepared, restriction digested with PstI and EcoRI, and purified (about 3950 base pairs) in a similar manner to the humanised 806.077 Fd fragment. Ligation mixes were prepared to clone the humanised 806.077 Fd gene fragment into the pCF004 vector, using a molar ratio of about 1 vector to 2.5 insert, and a final DNA concentration of about 2.5ng/μl, in the presence of T4 DNA ligase, 1mM ATP and enzyme buffer.

Following the ligation reaction, the DNA mixture was used to transform E.coli strain DH5α. Cell aliquots were plated on L-agar nutrient media containing 100μg/ml ampicillin as selection for plasmid vector, and incubated overnight at 37°C. A number of colonies were picked and used for mini-preparations of double stranded plasmid DNA. These DNA samples were analysed by restriction enzyme digestion, and a construct of the correct configuration identified. This plasmid containing the pre-pro-[A248S,G251T,D253K]HCPB-Linker-Fd(humanised 806.077) in pUC19 is known as pCF006.

e) Cloning pre-pro-[A248S,G251T,D253K]HCPB-linker-(humanised 806.077)Fd into pEE6 hCMV vector

Double stranded DNA of plasmid pCF006 (as documented above), was prepared using standard DNA technology (Qiagen plasmid kit or similar), and restriction digested with HindIII and EcoRI enzymes. DNA of the correct size, containing the fusion protein (about 2185 base pairs) was purified.

Double stranded DNA of plasmid vector pEE6 (as documented above) was prepared, restriction digested with HindIII and EcoRI, and purified (about 4775 base pairs) in a similar manner to the fusion protein. Ligation mixes were prepared to clone the humanised 806.077 Fd fusion protein into the pEE6 vector, using a molar ratio of about 1 vector to 2.5 insert, and a final DNA concentration of about 2.5ng/µl, in the presence of T4 DNA ligase, 1mM ATP and enzyme buffer. Following the ligation reaction the DNA mixture was used to transform E.coli strain DH5α. Cell aliquots were plated on L-agar nutrient media containing 100µg/ml ampicillin as selection for plasmid vector, and incubated overnight at 37°C. A number of colonies were picked and used for mini-preparations of double stranded plasmid DNA. These DNA samples were analysed by restriction enzyme digestion, and a construct of the correct configuration identified. This plasmid containing the pre-pro-[A248S,G251T,D253K]HCPB-Linker-Fd(humanised 806.077) in pEE6 is known as pCF007.

f) Cloning Humanised 806.077 light chain version 4 into pEE12 vector

Double stranded DNA of plasmid pNG3-VKss-806.077-HuVK4-HuCK-Neo, a construct consisting of the humanised 806.077 version HuVK4 with human CK cloned into vector pNG3 (see Examples 12-38), was prepared using standard DNA technology (Qiagen plasmid kit or similar), and restriction digested with HindIII and EcoRI enzymes. DNA of the correct size, containing the humanised 806.077 light chain (about 2022 base pairs) was purified. Double stranded DNA of plasmid vector pEE12 was prepared, restriction digested with HindIII and EcoRI, and purified (about 7085 base pairs) in a similar manner to the humanised 806.077 light chain. Ligation mixes were prepared to clone the humanised 806.077 light chain into the pEE12 vector, using a molar ratio of about 1 vector to 2.5 insert, and a final DNA concentration of about 2.5ng/µl, in the presence of T4 DNA ligase, 1mM ATP and enzyme buffer. Following the ligation reaction the DNA mixture was used to transform E.coli strain DH5α. Cell aliquots were plated on L-agar nutrient media containing 100µg/ml ampicillin as selection for plasmid vector, and incubated overnight at 37°C. A number of colonies were picked and used for mini-preparations of double stranded plasmid DNA. These DNA samples were analysed by restriction enzyme digestion, and a construct of

the correct configuration identified. This plasmid containing the humanised 806.077 light chain version 4 is known as pCF008/4.

g) Cloning CMVp-pre-pro-[A248S,G251T,D253K]HCPB-linker-(humanised 806.077)Fd into pCF008/4.

Double stranded DNA of plasmid pCF007 (as documented above), was prepared using standard DNA technology (Qiagen plasmid kit or similar), and restriction digested with BglII and SalI enzymes. Restriction enzyme BglII cuts the pCF007 plasmid prior to the start of the CMV MIE leader, promoter and gene for the fusion protein. Restriction enzyme SalI cuts about 520 base pairs after the stop codons of the mature protein. DNA of the correct size, containing the fusion protein (about 4844 base pairs) was purified. Double stranded DNA of plasmid vector pCF008/4 was prepared, restriction digested with BamHI and SalI, and purified (about 7436 base pairs) in a similar manner to the fusion protein. Ligation mixes were prepared to clone the [A248S,G251T,D253K]HCPB-linker-(humanised 806.077)Fd fusion gene into the pCF008/4 vector, using a molar ratio of about 1 vector to 2.5 insert, and a final DNA concentration of about 2.5ng/µl, in the presence of T4 DNA ligase, 1mM ATP and enzyme buffer. Following the ligation reaction the DNA mixture was used to transform E.coli strain DH5α. Cell aliquots were plated on L-agar nutrient media containing 100µg/ml ampicillin as selection for plasmid vector, and incubated overnight at 37°C. A number of colonies were picked and used for mini-preparations of double stranded plasmid DNA. These DNA samples were analysed by restriction enzyme digestion, and a construct of the correct configuration identified. This plasmid containing genes for pro-[A248S,G251T,D253K]HCPB-Linker-F(ab')$_2$(humanised 806.077 antibody) in the GS expression vector pEE12 is known as pCF009 and a plasmid map is shown in Figure 2. The DNA and amino acid sequences of the light chain HuVK4 are shown in SEQ ID NOs: 70 and 71. The DNA sequence of the pre-pro-[A248S,G251T,D253K]HCPB-linker-Fd(Humanised 806.077) is shown in SEQ ID NO: 124 and the corresponding amino acid sequence in SEQ ID NO: 125.

h) Expression of Pro-[mutant]HCPB-linker-F(ab')$_2$(humanised 806.077) from mouse myeloma cells.

The following method has been used for myeloma expression of all (D253K and G251T,D253K and A248S,G251T,D253K) mutant pro-HCPB enzyme fusion proteins.

The preferred mouse myeloma cell line is NS0 (Galfre and Milstein, 1981, Methods in Enzymol., 73, 3-46), and is available form the European Collection of Animal Cell Cultures, PHLS CAMR, Porton Down, Salisbury, Wiltshire, SP4 0JG (ECACC catalogue number 85110503). These cells were grown in Dulbecco's Modified Eagle Medium (DMEM; Gibco/BRL) containing 10% heat inactivated foetal calf serum (FCS).

For expression of pro-[A248S,G251T,D253K]HCPB-linker-F(ab')$_2$(humanised 806.077) two plasmids were used, pCF009 (described above) and pRc/RSV (from Invitrogen, Cat. no. V780-20) which contains the neomycin resistance gene for selection of G418 resistant stable cell lines. About 5µg of each plasmid (from 0.5 to 10µg) were used to transfect approximately $8x10^6$ NS0 cells by the method of lipofection (Felgner et al., in Methods: A Companion to Methods in Enzymology, 1993, 5, 67-75) which involves the cationic lipid mediated delivery of polynucleotides into eukaryotic cells. The cells were harvested by centrifugation, washed with serum free medium (30ml), resuspended in 800µl of medium and kept at 37°C in a tissue culture flask until the DNA was added. Serum-free medium (450µl) was mixed gently with LIPOFECTIN™ reagent (50µl) and incubated at room temperature for 30 to 45 minutes. This mixture was added to 500µl of medium containing the plasmid DNA mixture (in less than 100µl) and left at room temperature for 15 minutes. Serum free medium (600µl) was added to the plasmid DNA-LIPOFECTIN™ mixture, and the complex added to the cells which were incubated for about 5 hours at 37°C in a CO_2 incubator. The DNA containing medium was then replaced with normal DMEM medium (8ml) containing 10% FCS and the cells incubated overnight. The medium was then again replaced with normal DMEM medium (8ml) containing 10% FCS and the cells incubated as previously without selection for 24 hours. At the end of this period the medium was changed to DMEM containing 10% FCS and G418 selection (1.5 mg/ml), and the cells diluted (between 1 in 4 and 1 in 20) (approximately 0.5 to 1.5 x 10^6 cells per plate) in the same medium into micro-titre wells (150µl per well; 2 or more plates per dilution). The micro-titre plates were incubated for at least two weeks at 37°C in a CO_2 incubator and then checked regularly for viable clone formation.

Media from wells containing single viable clones was taken for testing and replaced with fresh media (containing G418). The removed media was tested for antibody binding to CEA in an ELISA (in the same manner as described in International Patent application Number WO 96/20011 Reference Example 5 part 1, except that the secondary antibody

solution was changed from anti-mouse to anti-human (goat anti-human Kappa light chain peroxidase conjugate, Sigma A7164). Positive samples for the CEA ELISA were also tested for [A248S,G251T,D253K]HCPB enzyme activity (as described above) following activation (removal of the pro domain from the fusion protein) by trypsin (700µg/ml in 50mM Tris-HCl and 150mM NaCl pH 7.6 at 4°C for 1 hour, the reaction being stopped by the addition of a five fold excess of soy bean trypsin inhibitor). A number of clones were identified which produced media that was positive for both 806.077 antibody binding to CEA and [A248S,G251T,D253K]HCPB enzyme activity. These were further tested by non-reducing Western blot analysis (in the same manner as described in International Patent Application Number WO 96/20011 Reference Example 5 part j, except that the antibody solution is changed from anti-mouse to anti-human (goat anti-human Kappa light chain peroxidase conjugate, Sigma A7164) to identify clones which produce predominately $F(ab')_2$(806.077) fusion protein. These clones were then expanded, tested for stable generation of the fusion protein over a number of generations, and the highest producers bulked up and stored frozen in liquid nitrogen using standard technology.

Amplification, high-level expression and fermentation of fusion proteins from NS0 myeloma cells was performed in a similar manner to that described by Bebbington et al. (1992) in Bio/Technology 10, 169-175. Fusion protein was purified, and the pro-sequence removed as described in Example 102.

Examples 76 to 101

Cloning and expression of other variants of pro-HCPB-Linker-(humanised 806.077)Fd + (humanised 806.077) light chain

The method for the generation of fusion proteins with other mutants of HPCB was similar to that detailed in Example 75 (above), with the exception that in part b. of Example 75 there was a substitution of [D253K]HCPB or [G251T,D253K]HCPB for [A248S,G251T,D253K]HCPB and the plasmid DNA used in the PCR reaction was pICI1713 (as described in International Patent application Number WO 96/20011, Example 15) or pZEN1860 (Reference Example 1) respectively. After cloning, identification, and sequence confirmation the resulting plasmid containing pre-pro-[D253K]HCPB-linker or pre-pro-[G251T,D253K]HCPB-linker and humanised 806.077 VH gene up to the PstI site (at

amino acid 5) in the pUC19 vector back ground was used in place of pCF004 in the subsequent cloning reactions.

The method for generation of fusion proteins with other CH1 domains was similar to that detailed in Example 75 (above), with the exception that in part c. of Example 75 there was a substitution of plasmids containing either humanised 806.077 VH version 1 with human IgG1 or IgG2 CH1 and hinge regions in place of 806.077-HuVH1-IgG3CH1' (SEQ ID NOs: 92 and 56 respectively). After cloning, identification, and sequence confirmation the resulting plasmid containing the IgG1 or IgG2 sequence was used in place of pCF005 in the subsequent cloning reactions.

The method for generation of fusion proteins with other variants of the humanised 806.077 light chain was similar to that detailed in Example 75 (above), with the exception that in part f. of Example 75 there was a substitution of plasmids containing either humanised 806.077 Lc version 1 or version 3 in place of 806.077-HuVK4-HuCK (SEQ ID NOs: 51 and 96 respectively). After cloning, identification, and sequence confirmation the resulting plasmid containing the alternative light chain sequence was used in place of pCF008/4 in the subsequent cloning reactions. The fusion protein variants for each Example (76 to 101) are shown in the following table.

Table

Example No.	Humanised Heavy chain	Humanised Light chain	Mutant HCPB Enzyme
76	HuVH1-HulgG3	HuVK4-HuCK	[D253K]HCPB
77	HuVH1-HulgG3	HuVK4-HuCK	[G251T,D253K]HCPB
78	HuVH1-HulgG3	HuVK1-HuCK	[A248S,G251T,D253K]HCPB
79	HuVH1-HulgG3	HuVK1-HuCK	[D253K]HCPB
80	HuVH1-HulgG3	HuVK1-HuCK	[G251T,D253K]HCPB
81	HuVH1-HulgG3	HuVK3-HuCK	[A248S,G251T,D253K]HCPB
82	HuVH1-HulgG3	HuVK3-HuCK	[D253K]HCPB
83	HuVH1-HulgG3	HuVK3-HuCK	[G251T,D253K]HCPB
84	HuVH1-HulgG1	HuVK4-HuCK	[A248S,G251T,D253K]HCPB
85	HuVH1-HulgG1	HuVK4-HuCK	[D253K]HCPB
86	HuVH1-HulgG1	HuVK4-HuCK	[G251T,D253K]HCPB
87	HuVH1-HulgG1	HuVK1-HuCK	[A248S,G251T,D253K]HCPB
88	HuVH1-HulgG1	HuVK1-HuCK	[D253K]HCPB

89	HuVH1-HulgG1	HuVK1-HuCK	[G251T,D253K]HCPB
90	HuVH1-HulgG1	HuVK3-HuCK	[A248S,G251T,D253K]HCPB
91	HuVH1-HulgG1	HuVK3-HuCK	[D253K]HCPB
92	HuVH1-HulgG1	HuVK3-HuCK	[G251T,D253K]HCPB
93	HuVH1-HulgG2	HuVK4-HuCK	[A248S,G251T,D253K]HCPB
94	HuVH1-HulgG2	HuVK4-HuCK	[D253K]HCPB
95	HuVH1-HulgG2	HuVK4-HuCK	[G251T,D253K]HCPB
96	HuVH1-HulgG2	HuVK1-HuCK	[A248S,G251T,D253K]HCPB
97	HuVH1-HulgG2	HuVK1-HuCK	[D253K]HCPB
98	HuVH1-HulgG2	HuVK1-HuCK	[G251T,D253K]HCPB
99	HuVH1-HulgG2	HuVK3-HuCK	[A248S,G251T,D253K]HCPB
100	HuVH1-HulgG2	HuVK3-HuCK	[D253K]HCPB
101	HuVH1-HulgG2	HuVK3-HuCK	[G251T,D253K]HCPB

Example 102

Purification of proteins containing 806.077 antibody sequences

Purification or enrichment of recombinant $F(ab')_2$ or antibody-enzyme fusion proteins may be achieved from myeloma cell, CHO cell or COS cell supernatants by several methods, used either singly or together. Purification of murine 806.077 $F(ab')_2$, chimeric 806.077 $F(ab')_2$ constructs and fully humanised 806.077 $F(ab')_2$ constructs, and antibody-enzyme fusion protein constructs incorporating these $F(ab')_2$ constructs were achieved by one or more of several different methods, affinity chromatography or anion exchange chromatography, or protein A / protein G chromatography. These techniques can also be applied to purification of 806.077 antibody - B7 fusions (see Example 104).

a) Antigen Affinity Chromatography

Carcinoembryonic antigen (CEA), to which the parent murine 806.077 antibody was raised, was immobilised on a column (using Pharmacia products). In brief, immobilisation was via a stable ester bond to Sepharose™ High Performance medium, NHS-activated prepacked in columns (HiTrap™); coupling of the CEA to the activated matrix was performed following the standard instructions provided with the product .

Preparation of a 1ml affinity column.

CEA stock solution (8mg/ml) was first diluted with coupling buffer (0.2M sodium hydrogen carbonate, 0.5M sodium chloride; pH8.3) to a final concentration of 0.5 mg/ml. A

new column was washed with 6ml of ice-cold 1mM HCl at a flow rate not exceeding 1ml/min. Immediately after, the CEA ligand (1ml at 0.5mg/ml) was injected onto the column. The column was sealed at both ends and left to stand for 30 minutes at room temperature. Excess active groups that had not coupled to the ligand were deactivated and any non-specifically bound ligand was washed out of the column by three rounds of alternating high and low pH washes. The buffers used were 0.5M ethanolamine, 0.5M sodium chloride (pH8.3) and 0.1M sodium acetate, 0.5M sodium chloride (pH 4.0). In each round of washes 6ml of each buffer was washed over the column matrix. Finally, the column was washed into storage buffer (0.05M Na_2HPO_4 , 0.1% NaN_3 , pH7.0).

Purification procedure

The cell culture supernatant containing the desired $F(ab')_2$ or fusion construct e.g. chimeric 806.077 $F(ab')_2$, humanised 806.077 $F(ab')_2$, or antibody-enzyme fusion protein was diluted 1:1 with phosphate buffered saline (pH 7.2) and passed over the 1ml affinity column at a flow rate of 1ml/min. The column had previously been equilibrated with phosphate buffered saline (pH7.2; 50mM sodium phoshate, 150mM sodium chloride). The column was washed with 10 column volumes of phosphate buffered saline after the cell supernatant had passed over it. Bound $F(ab')_2$ was eluted with 5 column volumes of 100mM sodium citrate (pH3.0), with 1ml fractions of the eluant being collected. Detection of the eluted $F(ab')_2$ was achieved by Western blot analysis using a suitable antibody peroxidase conjugate (an anti-human Kappa Light chain -peroxidase conjugate in the case of the fully humanised $F(ab')_2$, Sigma A-7164) and developing with hydrogen peroxide and 4-chloro-1-naphthol. Appropriate fractions were pooled and concentrated, using a centrifugal concentrator (Centricon™ 30), where necessary.

b) Anion Exchange Chromatography

Cell culture supernatant containing the required $F(ab')_2$ or fusion construct e.g. chimeric 806.077 $F(ab')_2$, humanised 806.077 $F(ab')_2$, or antibody-enzyme fusion protein was diafiltered into 50 mM Tris (using a stirred cell with a 10,000 molecular weight cut-off membrane) until the ionic strength of the solution was equivilant to the column equilibration buffer. The 40ml aliquot of the diafiltered supernatant was loaded on to a suitable column (Pharmacia Mono Q™ 10/10 HR) at 2ml/min. The column was previously equilibrated with 50mM Tris (pH8.0). Once the supernatant had passed over the column, the column was

washed back to baseline with the equilibration buffer. Bound material on the column was then eluted with a 0-50% buffer B (50mM Tris, 1M sodium chloride pH8.0) over 15 column volumes. Elution fractions were collected (4ml per fraction) and those containing the $F(ab')_2$ were identified by Western blot analysis using a suitable antibody peroxidase conjugate (an anti-human Kappa Light chain -peroxidase conjugate in the case of the fully humanised $F(ab')_2$, Sigma A-7164) and developing with hydrogen peroxide and 4-chloro-1-naphthol. Appropriate fractions were pooled and concentrated using a centrifugal concentrator (Centricon™ 30), where necessary.

c) Protein A and Protein G Purification

The cell culture supernatant containing the desired $F(ab')_2$ or fusion construct (e.g. 806.077 $F(ab')_2$, chimeric 806.077 IgG_1or IgG_2 or IgG_3; pro-HCPB-linker-806.077 $F(ab')_2$,806.077 $F(ab')_2$-HCPB) was diluted 1:1 with phosphate buffered saline before being loaded on to a column previously equilibrated in phosphate buffered saline (pH7.2). The column was washed with phosphate buffered saline, back to baseline, before the bound $F(ab')_2$ or fusion protein was eluted with 100mM sodium citrate (pH 3.0) in the case of the $F(ab')_2$ and 50mM glycine, 100mM sodium chloride (pH10.8) in the case of the fusion proteins. Elution fractions were collected and neutralised by the addition of 125µl 2M Tris per 1ml of elution volume. Those fractions containing the $F(ab')_2$ were pooled and concentrated where necessary using a centrifugal concentrator.

d) Pro-sequence cleavage:

For fusion proteins containing a covalently linked pro-sequence e.g.(Pro-HCPB-linker-806.077 $F(ab')_2$) the pro sequence was cleaved by incubation the fusion with trypsin. This procedure at a milligram (of fusion) scale involved the following. Trypsin was mixed with the fusion protein in a ratio of 1:1000 (trypsin:fusion). The mixture was incubated for 24 hours at room temperature (around 22°C), after which the cleavage of the pro sequence was complete. The fusion protein was separated from the pro sequence by recirculating the mixture in one of the generic chromatography purification or enrichment protocols.

Example 103

Assay of activity of antibody-enzyme fusion proteins containing mutant human CPB against Hipp-Glu prodrug analogues

Cell culture supernatants or purified antibody-enzyme fusion proteins containing mutants of human CPB (D253K; G252T,D253K; A248S,G251T,D253K: Examples 48-101) are assayed for their ability to convert hippuryl-L-glutamic acid (Hipp-Glu ; Reference Example 9 in International Patent Application Number WO 96/20011)) to hippuric acid using a HPLC based assay.

The reaction mixture (250 µl) contains either 4 µg of purified fusion protein or cell culture supernatant (used either neat or diluted with 0.025M Tris-HCl pH7.5; 125µl) and 0.5 mM Hipp-Glu in 0.025 M Tris-HCL, pH 7.5. Samples are incubated for 5 hr at 37°C. The reactions are terminated by the addition of 250 µl of 30% methanol, 70% phosphate buffer (50mM; pH 6.5), 0.2% trifluoroacetic acid and the amount of hippuric acid generated is quantified by HPLC (using a Hewlett Packard 1090 Series 11 with diode array system).

Samples (50 µl) are injected onto a column (25 cm; HICHROM™ Hi-RPB) and separated using a mobile phase of 15% methanol, 85% phosphate buffer (50mM; pH 6.5) at a flow rate of 1ml/min. The amount of product (hippuric acid) produced is determined from calibration curves generated with known amounts of hippuric acid (Sigma-H6375). Results are expressed as the percentage conversion of substrate into product at 37°C at times ranging from 30min-24h depending on rate of conversion.

For antibody-enzyme fusion proteins with an N-terminal proCPB, the pro domain is first removed by treatment with trypsin (700µg/ml) in 50mM Tris-HCl (pH7.6), 150mM NaCl at 4°C for 1h.

Example 104

Preparation of a human B7.1-humanised 806.077 F(ab')$_2$ fusion protein (hB7-806)

As in Reference Example 3, a fusion protein consisting of the signal sequence and extracellular domain of human B7.1 fused directly to the 5' coding region of the humanised 806.077 antibody Fd chain is constructed using PCR techniques. A HindIII-NheI fragment is created containing the natural signal sequence and extracellular domain of human B7.1 fused to the V_H region of a humanised 806.077 antibody heavy chain. This is cloned into a suitable

vector, for example pNG4-$V_H$ss-HuIgG2CH1' or pNG4-$V_H$ss-HuIgG3CH1' (see Examples 39-47) (replacing bases 1-423 in Seq.ID NO: 18), to create a human B7.1-humanised 806.077 Fd fusion gene. Co-expression of this fusion with a humanised 806.077 L chain (a suitable vector containing the VK4 version of humanised 806.077 light chain is pCF008/4; see Example 75) is then achieved after construction of a co-expression vector using expression systems such as those described herein. Such a vector is used to transfect NS0 myeloma cells and colonies selected on the presence of CEA binding activity in the culture supernatant. Other humanised sequences are described in Examples 39-47.

The hB7-806 fusion protein is expressed from a suitable cell line and purified using protein-A column as described in Reference Example 3 or one of the methods described in Example 102. It should be noted that purification methods other than protein-A columns are preferred for humanised 806.077 antibody fragments and fusion proteins thereof. The fusion protein can be tested for both antigen and receptor binding properties and T-cell co-stimulatory activity when bound to LS174T cells using assays set out in Reference Example 3.

Example 105

Preparation of chimeric and humanised 806.077 F(ab')$_2$-CPG2 conjugates

The procedure described in Example 5 was repeated with the murine F(ab')$_2$ protein replaced by one of the chimeric versions described in Example 8 or one of the humanised versions described in Examples 39-47.

Example 106

Preparation of humanised 806.077 Fab-CPG2 enzyme fusion protein.

Humanised 806.077 antibody and bacterial CPG2 enzyme fusion protein constructs are constructed using PCR methodology similar to that described for the construction of HuVK4 in Examples 12-38, in which specifically designed primers are used in a PCR reaction to amplify the antibody and enzyme gene components (such that the resulting DNA products contain overlapping complementary sequence) which are then joined via a further "splicing / joining" PCR reaction to make the complete antibody-enzyme fusion gene. The fusion protein is created by joining the 3' end of Fd humanised 806.077 antibody heavy chain gene to the 5' end of the CPG2 structural coding gene to create a Fab-CPG2 fusion protein coding gene. In

such a construct, the humanised 806.077 antibody heavy chain gene component may be terminated after residue K236 for the HuVH1-HuIgG1 Fd heavy chain (SEQ ID NO: 93), after residue Val 237 for the HuVH1-HuIgG2 Fd heavy chain (SEQ ID NO: 57) or after residue Val 237 heavy chain in the HuVH1-HuIgG3 Fd heavy chain (SEQ ID NO: 95) (thus, in each case, excluding any sequence pertaining to the hinge region) and may be joined to the first CPG2 residue positioned C-terminal to the signal sequence cleavage site (Minton et al (1984) Gene **31,** 31-38). However, in order to obtain optimal antibody binding and enzymatic properties, it is also envisaged that it may be desirable to incorporate additional residues at the junction between the two constituent components.

The fusion gene is then cloned into a suitable vector, for example pNG4-VHss-HuIgG2CH1' (NCIMB no. 40797), after the appropriate restiction enzyme digestion. isolation of the vector and fusion gene DNA fragment have been made thus replacing the original antibody gene with that of the fusion protein. Co-expression of the fusion with a humanised 806.077 light chain is then achieved after construction of a co-expression vector in a manner analogous to that described in Example 11. The co-expression vector is used to transfect NSO myeloma cells and colonies selected on the presence of CEA and Fd binding activity in the culture supernatant as previously described. The fusion protein can be purified using a Protein-A column and shown to have both antigen and enzymatic properties using standard test methodology.

Example 107

Further combination of humanised heavy and light chain variable regions based on light chain sequence VK4

The procedures described in Examples 12-38 are repeated with the humanised light chain variable sequence of VK4 (SEQ ID NO: 71) replaced by the modified sequence in which the tyrosine residue (Tyr) at position 35 of SEQ ID NO: 71 is replaced by a phenylalanine residue (Phe).

Example 108

Further combination f humanised heavy and light chain variable regions based n light chain sequence VK4

The procedures described in Examples 12-38 are repeated with the humanised light chain variable sequence of VK4 (SEQ ID NO: 71) replaced by the modified sequence in which the phenylalanine residue (Phe at position 72 of SEQ ID NO: 71 is replaced by a leucine residue (Leu).

Example 109

Further combination of humanised heavy and light chain variable regions based on light chain sequence VK4

The procedures described in Examples 12-38 are repeated with the humanised light chain variable sequence of VK4 (SEQ ID NO: 71) replaced by the modified sequence in which the tyrosine residue (Tyr) at position 35 and the phenylalanine residue (Phe) at position 72 of SEQ ID NO: 71 are replaced by a phenylalanine residue (Phe) and a leucine residue (Leu) respectively.

Example 110

Combination of humanised heavy chain variable regions and a chimeric light chain sequence

The procedures described in Examples 12-38 are repeated with the humanised light chain variable sequence of replaced by the chimeric sequence of SEQ ID NO: 17 described in Example 8.

Example 111-113

Expression of humanised F(ab')2 fragments with a modified light chain VK4 variable sequence

The procedures described in Examples 39-47 are repeated with the variable light chain sequence described in Example 107 used to make a replacement for the humanised light chain sequence of SEQ ID NO: 99 in which the tyrosine residue (Tyr) at position 57 of SEQ ID NO: 99 is replaced by a phenylalanine residue (Phe).

Example 111 is the combination of HuVH1-HuIgG1 and the modified SEQ ID NO: 99 described above.

Example 112 is the combination of HuVH1-HuIgG2 and the modified SEQ ID NO: 99 described above.

Example 113 is the combination of HuVH1-HuIgG3 and the modified SEQ ID NO: 99 described above.

Example 114-116

Expression of humanised F(ab')$_2$ fragments with a modified light chain VK4 variable sequence

The procedures described in Examples 39-47 are repeated with the variable light chain sequence described in Example 108 used to make a replacement for the humanised light chain sequence of SEQ ID NO: 99 in which the phenylalanine residue (Phe) at position 94 of SEQ ID NO: 99 is replaced by a leucine residue (Leu).

Example 114 is the combination of HuVH1-HuIgG1 and the modified SEQ ID NO: 99 described above.

Example 115 is the combination of HuVH1-HuIgG2 and the modified SEQ ID NO: 99 described above.

Example 116 is the combination of HuVH1-HuIgG3 and the modified SEQ ID NO: 99 described above.

Example 117-119

Expression of humanised F(ab')$_2$ fragments with a modified light chain VK4 variable sequence

The procedures described in Examples 39-47 are repeated with the variable light chain sequence described in Example 109 used to make a replacement for the humanised light chain sequence of SEQ ID NO: 99 in which the tyrosine residue (Tyr) at position 57 and the phenylalanine residue (Phe) at position 94 of SEQ ID NO: 99 is replaced by a phenylalanine residue (Phe) and leucine residue (Leu) respectively.

Example 117 is the combination of HuVH1-HuIgG1 and the modified SEQ ID NO: 99 described above.

Example 118 is the combination of HuVH1-HuIgG2 and the modified SEQ ID NO: 99 described above.

Example 119 is the combination of HuVH1-HuIgG3 and the modified SEQ ID NO: 99 described above.

Example 120-122

Expression of humanised $F(ab')_2$ fragments with a chimeric light chain sequence

The procedures described in Examples 39-47 are repeated with the chimeric light chain sequence described in Example 110 replacing the humanised light chain sequences used in Examples 39-47

Example 120 is the combination of HuVH1-HuIgG1 and the chimeric light chain sequence described above.

Example 121 is the combination of HuVH1-HuIgG2 and the chimeric light chain sequence described above.

Example 122 is the combination of HuVH1-HuIgG3 and the chimeric light chain sequence described above.

Example 123

Preparation of humanised fusion protein based on modified light chain VK4 sequence

The procedures described in Example 48 are repeated but with plasmid pEE14-806.077HuVK4-HuCK replaced by a plasmid containing the modified VK4 sequence of Examples 107 and 111 to 113.

Example 124

Preparation of humanised fusion protein based on modified light chain VK4 sequence

The procedures described in Example 48 are repeated but with plasmid pEE14-806.077HuVK4-HuCK replaced by a plasmid containing the modified VK4 sequence of Examples 108 and 114 to 116.

Example 125

Preparation of humanised fusion protein based on modified light chain VK4 sequence

The procedures described in Example 48 are repeated but with plasmid pEE14-806.077HuVK4-HuCK replaced by a plasmid containing the modified VK4 sequence of Examples 109 and 117 to 119.

Example 126

Preparation of humanised fusion protein based on a chimeric light chain VK4 sequence

The procedures described in Example 48 are repeated but with plasmid pEE14-806.077HuVK4-HuCK replaced by a plasmid containing the chimeric light chain sequence of Examples 110 and 120 to 122.

Example 127

Preparation of humanised fusion protein based on modified light chain VK4 sequence

The procedures described in Example 75 are repeated but with plasmid pCF008/4 replaced by a plasmid containing the modified VK4 sequence of Examples 107 and 111 to 113.

Example 128

Preparation of humanised fusion protein based on modified light chain VK4 sequence

The procedures described in Example 75 are repeated but with plasmid pCF008/4 replaced by a plasmid containing the modified VK4 sequence of Examples 108 and 114 to 116.

Example 129

Preparation of humanised fusion protein based on modified light chain VK4 sequence

The procedures described in Example 75 are repeated but with plasmid pCF008/4 replaced by a plasmid containing the modified VK4 sequence of Examples 109 and 117 to 119.

Example 130

Preparation f humanised fusion protein based n a chimeric light chain VK4 sequence

The procedures described in Example 75 are repeated but with plasmid pCF008/4 replaced by a plasmid containing the chimeric light chain sequence of Examples 110 and 120 to 122.

Reference Example 1

Preparation of gene sequence for [G251T,D253K]HCPB

The method of cloning [G251T,D253K]HCPB in E.coli was very similar to the method described in International Patent application Number WO 96/20011, Example 15. Again pICI266 was used as the cloning vector, but the starting material for PCR site directed mutagenesis was the [D253K]HCPB gene in plasmid pICI1713 (as described in International Patent Application Number WO 96/20011 Example 15). However, in this case site directed mutagenesis was used during the PCR amplification of the gene to change the codon at amino acid position 251 in the mature gene from Glycine to Threonine (GGC to ACT), the G251T change. Also during the generation of this mutation a number of other mutations were generated at the same (G251) site by using a mixture of oligonucleotides with codon changes at G251. Individual mutant genes were identified following transformation and hybridisation by sequencing across the mutation site, prior to complete gene sequencing. In this example only the oligonucleotide for introducing the G251T mutation will be considered. Two PCR mixtures were prepared, in a manner similar to that described in International Patent application Number WO 96/20011 Example 15. In the first reaction primers were CAN 00402 (SEQ ID NO: 116) and CAN 00734 (SEQ ID NO: 117). In the second reaction primers were CAN 00284 (SEQ ID NO: 118) and CAN 01076 (SEQ ID NO: 119). In both reactions the starting DNA was pICI1713.

Aliquots of the two PCR reactions were analysed for DNA of the correct size (about 750 and 250 base pairs) and estimation of concentration by agarose gel electrophoresis, and found to contain predominantly bands of the correct size. Another PCR was then set up using each of the first two PCR products, with the two end primers {CAN 00402 (SEQ ID NO: 116) and CAN 00284 (SEQ ID NO: 118)}. An aliquot of the PCR product was analysed for DNA of the correct size (about 1000 base pairs) by agarose gel electrophoresis and found to contain predominantly a band of the correct size. The remainder of the product from the reaction mix

was purified, the isolated DNA restriction digested with enzymes NcoI and EcoRI, and a band of the correct size (about 1000 base pairs) purified in a similar manner to that described in International Patent application Number WO 96/20011 Example 16.

pICI266 double stranded DNA was restriction digested with NcoI and EcoRI enzymes, and DNA of the correct size (about 5600 base pairs) was purified. Aliquots of both restricted and purified vector and insert DNA samples were checked for purity and concentration estimation using agarose gel electrophoresis compared with known standards. From these estimates ligation mixes were prepared to clone the HCPB gene into the pICI266 vector in a similar manner to that described in International Patent application Number WO 96/20011 Example 16.

Following the ligation reaction the DNA mixture was used to transform E.coli strain DH5α. colonies were picked and tested by hybridisation. A number of the clones were then taken for plasmid DNA preparation. and were sequenced over the region of PCR mutation in order to identify clones with the G251T change in a manner similar to that described in International Patent application Number WO 96/20011 Example 16. From the sequencing results a clone containing a plasmid with the required [G251T:D253K]HCPB gene sequence was selected, and the plasmid called pZEN1860.

Reference Example 2

Preparation of gene sequence for [A248S,G251T,D253K]HCPB

The method of cloning [A248S,G251T,D253K]HCPB in E.coli was very similar to the method described in Reference Example 1. The starting material for the PCR site directed mutagenesis was the [G251T,D253K]HCPB gene in plasmid pZEN1860 (described in Reference Example 1) in place of pICI1713. However, in this case site directed mutagenesis was used during the PCR amplification of the gene to change the codon at amino acid position 248 in the mature gene from alanine to serine (GCT to TTC), the A248S change. Two PCR mixtures were prepared, in a manner similar to that described in Reference Examples 1. In the first reaction primers were CAN 00402 (SEQ ID NO: 116) and CAN 00720 (SEQ ID NO: 120). In the second reaction primers were CAN 00284 (SEQ ID NO: 118) and CAN 00726 (SEQ ID NO: 121). In both reactions the starting DNA was pZEN1860.

Methods of PCR, cloning, expression and identification were the same as for Reference Example 1. From the sequencing results a clone containing a plasmid with the

required [A248S,G251T,D253K]HCPB gene sequence was selected, and the plasmid called pZEN1921.

Reference Example 3

Preparation and characterisation of a human B7.1-murine A5B7 F(ab')$_2$ fusion protein (AB7)

Methods for the preparation, purification and characterisation of recombinant murine A5B7 F(ab')$_2$ antibody have been published (WO 96/20011, Reference Example 5). The cDNA sequence for human B7.1 antigen (also called CD80) has been isolated and described (Freeman G.J *et al*, Journal of Immunology, 1989, **143**, 2714-2722). In this Example "AB7" refers to human B7.1-murine A5B7 F(ab')$_2$ fusion protein and "A5B7" refers to the anti-CEA antibody termed A5B7.

Using a PCR based strategy we isolated the natural signal sequence and extracellular domain of human B7.1 (encoding amino-acids 1-242) from cDNA prepared from cultured Raji cells (ATCC No. CCL 86) and fused it directly upstream from the mature 5' coding sequence of the murine A5B7 Fd fragment. This involved isolation of the B7.1 sequence with PCR primers 187/96 and 204/96 (SEQ ID NOS: 126 and 127) and a partial A5B7 Fd sequence with PCR primers 203/96 and 205/96 (SEQ ID NOS: 128 and 129). After purification of the PCR products they were mixed in approximately equimolar amounts and fused by PCR with primers 187/96 and 205/96. The resulting PCR product was purified, digested with HindIII and BstEII (New England Biolabs (UK) Ltd., Wilbury Way, Hitchin, SG4 OTY) and cloned into the HindIII-BstEII region of pAF1 using standard procedures to create the full length human B7.1-murine A5B7 Fd fusion. This fusion gene (SEQ ID NO: 130 - 131) was cloned as a EcoRI-HindIII fragment into the GS-system™ expression vector pEE6 (Celltech Biologics, Bath Road, Slough, SL1 4EN) according to the protocols described in WO 96/20011, Reference Example 5, to generate vector pAB7.1.

A BglII-SalI fragment containing the B7.1-A5B7 Fd expression cassette was then cloned between the BglII and SalI sites of the vector pAF6 previously described to generate a vector (pAB7.2) capable of co-expressing the fusion protein and the A5B7 L chain. The vector pAB7.2 was then used to transform NS0 myeloma cells and colonies selected on their ability to grow in the absence of glutamine. Cell lines expressing the fusion protein were identified by determination of CEA binding activity in the culture supernatant using the

ELISA described. A cell line expressing suitable levels of fusion protein (1D4) was selected for purification and characterisation of the AB7 fusion protein.

Purification and characterisation of the AB7 fusion protein

The secreted recombinant B7.1(35-242)-A5B7 $F(ab)_2$, AB7, material was purified from culture supernatant using a Protein-A agarose matrix such as for example Protein-A Sepharose 4 fast flow as manufactured by Pharmacia (Pharmacia Biotech, 23 Grosvenor Rd, St Albans, Herts, AL1 3AW). The matrix was washed with 2x 8 matrix volumes of binding buffer (3M NaCl, 1.5M Glycine, pH 8.9). The culture supernatant containing AB7 was diluted 1:1 with the binding buffer. The washed matrix was added to the diluted culture supernatant (1ml settled volume of matrix per 40ml of diluted supernatant) and incubated at 4°C for 2hrs with moderate shaking. The matrix was spun down by centrifugation and approx. 75% of the supernatant carefully poured off. The matrix was then resuspended in the residual supernatant and the resulting slurry packed into a column. The column was washed with 5-6 column volumes of 150mM NaCl, 10mM NaH_2PO_4, pH7.4. The buffer was then changed to 100mM NaCitrate pH2.8 and elution fractions collected. These fractions were titrated to approximately pH7.0 by the addition of 2M Tris buffer pH.8.5. The elution fractions were analysed by non-reducing SDS-PAGE and the peak AB7 fraction(s) retained as the product.

N-Terminal Sequencing

A sample of AB7 was run on reducing SDS-PAGE and blotted onto PVDF (polyvinylidene difluoride) membrane (equipment, gels, blotting membrane and methods from NOVEX, 4202 Sorrento Valley Blvd, San Diego, CA 92121, USA.). The protein bands were stained with Coomassie blue and the band at approximately 70kDa (i.e. B7.1-Fd fusion) was N-terminally sequenced (Applied Biosystems, 494 Protein Sequencer (Perkin Elmer, ABI division, Kelvin close, Birchwood Science Park North, Warrington, WA3 7PB.) The sequence obtained matched the expected sequence for mature B7 (ie. after leader sequence cleavage from amino-acid 35 in SEQ.ID NO: 131, Val Ile His Val etc.).

BIAcore Analysis

AB7 was analysed using BIAcore surface plasmon resonance equipment made by Biacore (23 Grosvenor Rd, St. Albans, Herts., AL1 3AW, UK.) according to methods for BIAcore analysis of the CD80/CTLA-4 interaction taken from Greene JL, Leytze GM, Emswiler J, Peach R, Bajorath J, Cosand W, and Linsley PS. (1996) J. Biol. Chem. **271**,

26762-26771. Samples of the purified AB7 product were injected over both a CTLA4-Ig amine coupled surface and a blank (control) amine coupled surface. Binding could clearly be seen to the CTLA4-Ig surface compared to the control surface (see Figure 3). Binding could also be demonstrated between CTLA4-Ig and AB7 when the CTLA4-Ig was injected over an amine coupled AB7 surface.

Combined with the data from the anti-CEA ELISA these data confirm that the purified AB7 fusion protein has the biological properties of both component parts, namely antigen and receptor binding activities.

Co-stimulatory activity of the AB7 fusion protein

The ability of the AB7 fusion protein to provide a co-stimulatory signal to T cells when bound to CEA expressing tumour cells was tested using an adaptation of a co-stimulation assay format previously described (Jenkins et al. (1991) J. Immunol. 147:2461). CEA expressing LS174T colo-rectal tumour cells (fixed using 0.5% paraformaldehyde for 5 minutes at room temperature) were incubated with 10μg/ml of the AB7 fusion protein (2 hours rotating at 4°C in RPMI 1640 medium (Gibco. Life Technologies, Paisley, Scotland), containing 0.5% human serum (Sigma AB, Sigma Chemical Co, Dorset, UK.). The cells were washed twice prior to use and binding of the fusion protein confirmed using a fluoroscein isothiocyanate (FITC)- conjugated goat-anti-mouse Ig (Becton-Dickinson UK Ltd, Oxford) and flow cytometry (Facscan, Becton Dickinson). To allow the use of unprimed human T cells in the assay, the T cell receptor (TCR) stimulus was provided by an anti T cell receptor antibody (anti-CD3 antibody, OKT-3 Orthoclinical Diagnostics, Amersham, UK) previously coated onto the wells of a 96 well plate. OKT-3 was immobilised by incubating purified antibody (2μg/ml in bicarbonate coating buffer, pH 9.6 (preformed capsule, Sigma)) overnight at 4° C in 96 well flat bottomed microtitre plates (Costar Corporation, Cambridge, MA, USA), which were then washed three to four times with PBS. Purified peripheral T cells (from negatively depleted (i.e. pulling out components other than T cells) from donor human blood using magnetic beads (Dynabeads, Dynal A.S, Oslo, Norway) were added to the wells at 2 x 10^5/well in 50μl of RPMI 1640 medium containing 5% human serum. The fusion protein bound LS174T cells were added to the wells at 5 x 10^4/well in 50μl of RPMI 1640 medium plus 5% human serum. Finally the volume in all wells was made up to 200μl using RPMI 1640 medium plus 5% human serum. Cultures were pulsed with 1.25 μCi of [^{3}H] thymidine (Amersham International) after 48 hours and harvested 16 hours later with a semi-automated

cell harvester (TomTec harvester, Wallac UK.). The incorporation of [^{3}H] thymidine into DNA was quantitated using liquid scintillation counting (Betaplate Scint and Betaplate counter, Wallac UK.). Data from a typical costimulation assay is displayed in the Table below.

Table: Co-stimulation data

	αCD3 coated onto wells @ 2μg/ml (cpm)
T cells alone	3582
T cells + αCD28	28178
T cells + LS174T	12303
T cells + LS174T + αCD28	25759
T cells + LS174T/fusion protein	41755

αCD3 = anti-CD3 antibody; αCD28 = anti-CD28 antibody

Unprimed T-cells require both T-cell receptor and co-stimulatory signals. In the assay the T-cell receptor signal is provided by αCD3 antibody. Providing co-stimulation via αCD28 (Becton-Dickinson used at 0.6μg/ml) stimulates uptake of [^{3}H] thymidine over 8 fold compared to αCD3 alone. The presence of tumour cells has no significant effect on this stimulation. Providing the co-stimulatory signal by AB7 fusion protein bound to tumour cells stimulates uptake of [^{3}H] thymidine by more than 3 fold over that given by tumour cells alone and over 11 fold higher than that seen in the absence of co-stimulation. The apparent stimulation provided by tumour cells alone may arise from residual accessory cells in the purified T-cell population. Similar increases in T cell proliferation were consistently observed in wells containing tumour cell bound fusion protein in each of 5 assays carried out compared with wells containing T cells and unbound tumour cells.

Reference Example 4

Preparation of IgG3-pBSIIKS+

This example describes the preparation of a vector containing a gene for the human IgG3 heavy chain constant and hinge region.

A gene containing the sequence shown in SEQ ID NO: 115 [this contains a sequence (residues 8 to 508) that is similar to SEQ ID NO: 25, but with residues 312 and 501 of SEQ ID NO: 25 changed to C and G respectively], was prepared by PCR by a method similar to that described by Jayaraman et al. (1991) Proc. Natl. Acad. Sci USA 88, 4084-4088.

The gene was made in two parts, known as IgG3A and IgG3B. These were cloned separately into the SacI and XmaI sites of pBluescript KS+ (Stratagene Cloning Systems) to give vectors IgG3A-pBSIIKS+ clone A7 and IgG3B-pBSIIKS+ clone B17 respectively. IgG3A was made to extend past the PmaCI restriction site (CACGTG at positions 334-339 in SEQ ID NO: 115). Similarly, IgG3B was made such that the 5' end of the sequence was upstream of the PmaCI restriction site. To obtain the desired IgG3 gene sequence, the intermediate IgG3A and IgG3B vectors were cut with AflIII and PmaCI. The vector fragment (2823bp) from IgG3A-pBSIIKS+ clone A7, and insert fragment from IgG3B-pBSIIKS+ clone B17 (666bp) were isolated by electrophoresis in a 1% agarose gel and purified. The fragments were ligated and the ligation mix used to transform E. coli strain DH5α. Clones containing the required gene were identified by digestion of isolated DNA with SacI and XmaI to give a 520bp fragment. The sequence of the insert was confirmed by DNA sequence analysis and clone number F3 was designated IgG3-pBSIIKS+.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: ZENECA LIMITED

(B) STREET: 15 STANHOPE GATE

(C) CITY: LONDON

(E) COUNTRY: UNITED KINGDOM

(F) POSTAL CODE (ZIP): W1Y 6LN

(G) TELEPHONE: 0171 304 5000

(H) TELEFAX: 0171 304 5151

(I) TELEX: 0171 834 2042

(ii) TITLE OF INVENTION: PROTEINS

(iii) NUMBER OF SEQUENCES: 131

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGAAGCTTGA AGATGGATAC AGTTGGTGCA GC 32

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGAAGCTTAG ACAGATGGGG GTGTCGTTTT G 31

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn
20 25 30

Tyr Met

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GACATTCAGC TGACCCAGTC TCCA 24

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GACATTGAGC TCACCCAGTC TCCA 24

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AGGTSMARCT GCAGSAGTCW GG 22

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ACTAGTGGAA TTCAGTGTGA GGTSCARCTG CAGCARTCWG G 41

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GACATTGAGC TCACCCAGTC TCCAGCAATC ATGTCTGCAT CTCCAGGGGA GAAGGTCACC 60

ATAACCTGCA GTGCCAGCTC AAGTGTAACT TACATGCACT GGTTCCAGCA GAAGCCAGGC 120

ACTTCTCCCA AACTCTGGAT TTATAGCACA TCCAACCTGG CTTCTGGAGT CCCTGCTCGC 180

TTCAGTGGCA GTGGATCTGG GACCTCTTAC TCTCTCACAA TCAGCCGAAT GGAGGCTGAA 240

GATGCTGCCA CTTATTACTG CCAGCAAAGG AGTACTTACC CGCTCACGTT CGGTGCTGGG 300

ACCAAGCTGG AGCTGAAACG GGCTGATGCT GCACCAACTG TATCCATCTT CAAGCTT 357

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Asp	Ile	Glu	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Met	Ser	Ala	Ser	Pro	Gly
1				5					10					15	
Glu	Lys	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Val	Thr	Tyr	Met
			20					25					30		
His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Thr	Ser	Pro	Lys	Leu	Trp	Ile	Tyr
		35					40					45			
Ser	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg	Met	Glu	Ala	Glu
65					70					75					80
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Thr	Tyr	Pro	Leu	Thr
				85					90					95	
Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	Arg	Ala				
			100					105							

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GAGGTGCAGC TGCAGCARTC WGGGGCAGAG CTTGTGAGGT CAGGGGCCTC AGTCAAGTTG 60

TCCTGCACAG CTTCTGGCTT CAACATTAAA GACAACTATA TGCACTGGGT GAAGCAGAGG 120

CCTGAACAGG GCCTGGAGTG GATTGCATGG ATTGATCCTG AGAATGGTGA TACTGAATAT 180

GCCCCGAAGT TCCGGGGCAA GGCCACTTTG ACTGCAGACT CATCCTCCAA CACAGCCTAC 240

CTGCACCTCA GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTACTGTCA TGTCCTGATC 300

TATGCTGGTT ATTTGGCTAT GGACTACTGG GGTCAAGGAA CCTCAGTCGC CGTCTCCTCA 360

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn
20 25 30

Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Ala Asp Ser Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu His Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Ser Val Ala Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AAGCTTTCCC GCGGGGACAT TGAGCTCACC CAGTCTCCA 39

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

AAGCTTCTCG AGCTTGGTCC CAGCACCGAA 30

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AAGCTTGGAA TTCAGTGTGA GGTGCAGCTG CAGCAG 36

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

AAGCTTCGAG CTCACGGCGA CTGAGGTTCC TTG 33

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 705 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ATGGATTTTC AAGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCTTCAGT CATAATGTCC 60

CGCGGGGACA TTGAGCTCAC CCAGTCTCCA GCAATCATGT CTGCATCTCC AGGGGAGAAG 120

GTCACCATAA CCTGCAGTGC CAGCTCAAGT GTAACTTACA TGCACTGGTT CCAGCAGAAG 180

CCAGGCACTT CTCCCAAACT CTGGATTTAT AGCACATCCA ACCTGGCTTC TGGAGTCCCT 240

GCTCGCTTCA GTGGCAGTGG ATCTGGGACC TCTTACTCTC TCACAATCAG CCGAATGGAG 300

GCTGAAGATG CTGCCACTTA TTACTGCCAG CAAAGGAGTA CTTACCCGCT CACGTTCGGT 360

GCTGGGACCA AGCTCGAGAT CAAACGGACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 420

CCATCTGATG AGCAGTTGAA ATCTGGAACT GCCTCTGTTG TGTGCCTGCT GAATAACTTC 480

TATCCCAGAG AGGCCAAAGT ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 540

CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCCTG 600

ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 660

GGCCTGAGTT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGT 705

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg Gly Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile
20 25 30

Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser
35 40 45

Ser Ser Val Thr Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser
50 55 60

Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95

Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg
100 105 110

Ser Thr Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

ATGAAGTTGT GGCTGAACTG GATTTTCCTT GTAACACTTT TAAATGGAAT TCAGTGTGAG 60

GTGCAGCTGC AGCARTCAGG GGCAGAGCTT GTGAGGTCAG GGGCCTCAGT CAAGTTGTCC 120

TGCACAGCTT CTGGCTTCAA CATTAAAGAC AACTATATGC ACTGGGTGAA GCAGAGGCCT 180

GAACAGGGCC TGGAGTGGAT TGCATGGATT GATCCTGAGA ATGGTGATAC TGAATATGCC 240

CCGAAGTTCC GGGGCAAGGC CACTTTGACT GCAGACTCAT CCTCCAACAC AGCCTACCTG 300

CACCTCAGCA GCCTGACATC TGAGGACACT GCCGTCTATT ACTGTCATGT CCTGATCTAT 360

GCTGGTTATT TGGCTATGGA CTACTGGGGT CAAGGAACCT CAGTCGCCGT GAGCTCGGCT 420

AGCACCAAGG GACCATCGGT CTTCCCCCTG GCCCCCTGCT CCAGGAGCAC CTCCGAGAGC 480

ACAGCCGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 540

AACTCAGGCG CTCTGACCAG CGGCGTGCAC ACCTTCCCGG CTGTCCTACA GTCCTCAGGA 600

CTCTACTCCC TCAGCAGCGT CGTGACGGTG CCCTCCAGCA ACTTCGGCAC CCAGACCTAC 660

ACCTGCAACG TAGATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGACAGT TGAGCGCAAA 720

TGTTGTGTCG AGTGCCCACC GTGCCCGGCG CCACCTGTGG CCGGC 765

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly
1 5 10 15

Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

Ser Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
35 40 45

Lys Asp Asn Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu
50 55 60

Glu Trp Ile Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala
65 70 75 80

Pro Lys Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Ser Ser Ser Asn
85 90 95

Thr Ala Tyr Leu His Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr
115 120 125

Trp Gly Gln Gly Thr Ser Val Ala Val Ser Ser Ala Ser Thr Lys Gly
130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
195 200 205

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
210 215 220

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
225 230 235 240

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
245 250 255

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Asn Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro
115 120

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 369 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG 60

GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG 120

TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA 180

GGACTCTACT CCCTCAGCAG CGTGGTGACT GTGCCCTCCA GCAGCTTGGG CACCCAGACC 240

TACATCTGCA ACGTGAATCA CAACCCCAGC AACACCAAGG TCGACAAGAA AGTTGAGCCC 300

AAATCTTGTG ACAAGACGCA CACGTGCCCG CCGTGCCCGG CTCCGGAACT GCTGGGTGGC 360

CCGTAATAG 369

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
100 105 110

Pro Val Ala Gly
115

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GCTAGCACCA AGGGACCATC GGTCTTCCCC CTGGCCCCCT GCTCCAGGAG CACCTCCGAG 60

AGCACAGCCG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG 120

TGGAACTCAG GCGCTCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA 180

GGACTCTACT CCCTCAGCAG CGTCGTGACG GTGCCCTCCA GCAACTTCGG CACCCAGACC 240

TACACCTGCA ACGTAGATCA CAAGCCCAGC AACACCAAGG TGGACAAGAC AGTTGAGCGC 300

AAATGTTGTG TCGAGTGCCC ACCGTGCCCG GCGCCACCTG TGGCCGGC 348

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
100 105 110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
115 120 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
130 135 140

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145 150 155 160

Ala Pro Glu Leu Leu Gly Gly
165

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GCTAGCACCA AGGGCCCATC GGTCTTCCCC CTGGCGCCCT GCTCCAGGAG CACCTCTGGG 60

GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG 120

TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA 180

GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC 240

TACACCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAG AGTGGAGCTG 300

AAAACCCCAC TTGGTGACAC AACTCACACG TGCCCTAGGT GTCCTGAACC TAAATCTTGT 360

GACACACCTC CCCCGTGCCC ACGGTGCCCA GAGCCCAAAT CTTGCGACAC GCCCCCACCG 420

TGTCCCAGAT GTCCTGAACC AAAGAGCTGT GACACTCCAC CGCCCTGCCC GAGGTGCCCA 480

GCACCTGAAC TCCTGGGAGG A 501

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Ser Ala Ser Ser Ser Val Thr Tyr Met His
1 5 10

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Ser Thr Ser Asn Leu Ala Ser
1 5

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Gln Gln Arg Ser Thr Tyr Pro Leu Thr
1 5

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Asp Asn Tyr Met His
1 5

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Phe Asn Ile Lys Asp Asn Tyr Met His
1 5

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe Arg
1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TCGAGAGATC TAAGCTTCCG CGGGAATTCC TCGAGGAGCT CCCCGGGGGA TCCGTCGACT 60

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CTAGAGTCGA CGGATCCCCC GGGGAGCTCC TCGAGGAATT CCCGCGGAAG CTTAGATCTC 60

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

AAGCTTCCCG GGTATTAAAG CAGAACTTG 29

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ACTAGTGGAT CCCAGACATG ATAAGATAC 29

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GGTCTATATA AGCAGAGCTG TCTGGCTAAC TAGAGAACC 39

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GGTTCTCTAG TTAGCCAGAC AGCTCTGCTT ATATAGACC 39

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

GGACTTTCCT ACTTGGCAG 19

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GGCAACTAGA AGGCACAGTC 20

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

AGCTTGCCGC CACCATGGAT TTTCAAGTGC AGATTTTCAG CTTCCTGCTA ATCAGTGCTT 60

CAGTCATAAT GTCCCGC 77

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GGGACATTAT GACTGAAGCA CTGATTAGCA GGAAGCTGAA AATCTGCACT TGAAAATCCA 60

TGGTGGCGGC A 71

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

AGCTTGCCGC CACCATGAAG TTGTGGCTGA ACTGGATTTT CCTTGTAACA CTTTTAAATG 60

G 61

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

AATTCCATTT AAAAGTGTTA CAAGGAAAAT CCAGTTCAGC CACAACTTCA TGGTGGCGGC 60

A 61

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

AAGCTTCTCG AGATCAAACG GACTGTGGCT GCACCATCTG TCTTCATCTT CCCGCCATCT 60

GATGAGCAGT TGAAATCTGG AACTGCCTCT GTTGTGTGCC TGCTGAATAA CTTCTATCCC 120

AGAGAGGCCA AAGTACAGTG GAAGGTGGAT AACGCCCTCC AATCGGGTAA CTCCCAGGAG 180

AGTGTCACAG AGCAGGACAG CAAGGACAGC ACCTACAGCC TCAGCAGCAC CCTGACGCTG 240

AGCAAAGCAG ACTACGAGAA ACACAAAGTC TACGCCTGCG AAGTCACCCA TCAGGGCCTG 300

AGTTCGCCCG TCACAAAGAG CTTCAACAGG GGAGAGTGTT AATAGCCCGG GACTAGT 357

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGAAGCTTGA GCTCGGCTAG CACCAAGGGA CCATCGGTCT TCCCCCTGGC CCCCTGCTCC 60

AGGAGCACCT CCGAGAGCAC AGCCGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA 120

CCGGTGACGG TGTCGTGGAA CTCAGGCGCT CTGACCAGCG GCGTGCACAC CTTCCCGGCT 180

GTCCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTCG TGACGGTGCC CTCCAGCAAC 240

TTCGGCACCC AGACCTACAC CTGCAACGTA GATCACAAGC CCAGCAACAC CAAGGTGGAC 300

AAGACAGTTG AGCGCAAATG TTGTGTCGAG TGCCCACCGT GCCCGGCGCC ACCTGTGGCC 360

GGCTAATAGC CCGGGACTAG T 381

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

AAGCTTTCCC GCGGCGACAT CCAGATGACC CAGAGCCCAA GCAGCCTGAG CGCTAGCGTG 60

GGTGACAGAG TGACCATCAC GTGTAGTGCC AGCTCAAGTG TAACTTACAT GCACTGGTAC 120

CAGCAGAAGC CAGGTAAGGC TCCAAAGCTG CTGATCTACA GCACATCCAA CCTGGCTTCT 180

GGTGTGCCAA GCAGATTCTC CGGAAGCGGT AGCGGCACCG ACTACACCTT CACCATCAGC 240

AGCCTCCAGC CAGAGGATAT CGCCACCTAC TACTGCCAGC AGAGGAGTAC TTACCCGCTC 300

ACGTTCGGCC AAGGGACCAA GCTCGAGATC AAACGGACTA GT 342

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GACATCCAGA TGACCCAGAG CCCAAGCAGC CTGAGCGCTA GCGTGGGTGA CAGAGTGACC 60

ATCACGTGTA GTGCCAGCTC AAGTGTAACT TACATGCACT GGTACCAGCA GAAGCCAGGT 120

AAGGCTCCAA AGCTGCTGAT CTACAGCACA TCCAACCTGG CTTCTGGTGT GCCAAGCAGA 180

TTCTCCGGAA GCGGTAGCGG CACCGACTAC ACCTTCACCA TCAGCAGCCT CCAGCCAGAG 240

GATATCGCCA CCTACTACTG CCAGCAGAGG AGTACTTACC CGCTCACGTT CGGCCAAGGG 300

ACCAAGCTCG AGATCAAACG G 321

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 705 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

ATGGATTTTC AAGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCTTCAGT CATAATGTCC 60

CGCGGCGACA TCCAGATGAC CCAGAGCCCA AGCAGCCTGA GCGCTAGCGT GGGTGACAGA 120

GTGACCATCA CGTGTAGTGC CAGCTCAAGT GTAACTTACA TGCACTGGTA CCAGCAGAAG 180

CCAGGTAAGG CTCCAAAGCT GCTGATCTAC AGCACATCCA ACCTGGCTTC TGGTGTGCCA 240

AGCAGATTCT CCGGAAGCGG TAGCGGCACC GACTACACCT TCACCATCAG CAGCCTCCAG 300

CCAGAGGATA TCGCCACCTA CTACTGCCAG CAGAGGAGTA CTTACCCGCT CACGTTCGGC 360

CAAGGGACCA AGCTCGAGAT CAAACGGACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 420

CCATCTGATG AGCAGTTGAA ATCTGGAACT GCCTCTGTTG TGTGCCTGCT GAATAACTTC 480

TATCCCAGAG AGGCCAAAGT ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 540

CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCCTG 600

ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 660

GGCCTGAGTT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGT 705

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser
35 40 45

Ser Ser Val Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
50 55 60

Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg
100 105 110

Ser Thr Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GAAGCTTGGA ATTCAGTGTG AGGTGCAGCT GCAGCAGAGC GGTCCAGGTC TCGTACGGCC 60

TAGCCAGACC CTGAGCCTCA CGTGCACCGC ATCTGGCTTC AACATTAAGG ACAATTACAT 120

GCACTGGGTG AGACAGCCAC CTGGACGAGG CCTTGAGTGG ATTGGATGGA TTGACCCTGA 180

GAATGGTGAC ACTGAGTACG CACCTAAGTT TCGCGGCCGC GTGACAATGC TGGCAGACAC 240

TAGTAAGAAC CAGTTCAGCC TGAGACTCAG CAGCGTGACA GCCGCCGACA CCGCGGTCTA 300

TTATTGTCAC GTCCTGATAT ACGCCGGGTA TCTGGCAATG GACTACTGGG GCCAAGGGAC 360

CCTCGTCACC GTGAGCTCGA CTAGT 385

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60

ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

CCTGGACGAG GCCTTGAGTG GATTGGATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180

GCACCTAAGT TTCGCGGCCG CGTGACAATG CTGGCAGACA CTAGTAAGAA CCAGTTCAGC 240

CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn
20 25 30

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

ATGAAGTTGT GGCTGAACTG GATTTTCCTT GTAACACTTT TAAATGGAAT TCAGTGTGAG 60

GTGCAGCTGC AGCAGAGCGG TCCAGGTCTC GTACGGCCTA GCCAGACCCT GAGCCTCACG 120

TGCACCGCAT CTGGCTTCAA CATTAAGGAC AATTACATGC ACTGGGTGAG ACAGCCACCT 180

GGACGAGGCC TTGAGTGGAT TGGATGGATT GACCCTGAGA ATGGTGACAC TGAGTACGCA 240

CCTAAGTTTC GCGGCCGCGT GACAATGCTG GCAGACACTA GTAAGAACCA GTTCAGCCTG 300

AGACTCAGCA GCGTGACAGC CGCCGACACC GCGGTCTATT ATTGTCACGT CCTGATATAC 360

GCCGGGTATC TGGCAATGGA CTACTGGGGC CAAGGGACCC TCGTCACCGT GAGCTCGGCT 420

AGCACCAAGG GACCATCGGT CTTCCCCCTG GCCCCCTGCT CCAGGAGCAC CTCCGAGAGC 480

ACAGCCGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 540

AACTCAGGCG CTCTGACCAG CGGCGTGCAC ACCTTCCCGG CTGTCCTACA GTCCTCAGGA 600

CTCTACTCCC TCAGCAGCGT CGTGACGGTG CCCTCCAGCA ACTTCGGCAC CCAGACCTAC 660

ACCTGCAACG TAGATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGACAGT TGAGCGCAAA 720

TGTTGTGTCG AGTGCCCACC GTGCCCGGCG CCACCTGTGG CCGGC 765

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly
1 5 10 15

Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg
20 25 30

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
35 40 45

Lys Asp Asn Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
50 55 60

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala
65 70 75 80

Pro Lys Phe Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn
85 90 95

Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
100 105 110

Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr
115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
195 200 205

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
210 215 220

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
225 230 235 240

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
245 250 255

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GGCGACATCC AGCTGACCCA GAGCCCAAGC AGCCTGAGCG 40

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

CTAGCGCTCA GGCTGCTTGG GCTCTGGGTC AGCTGGATGT CGCCGC 46

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GACATCCAGC TGACCCAGAG CCCAAGCAGC CTGAGCGCTA GCGTGGGTGA CAGAGTGACC 60

ATCACGTGTA GTGCCAGCTC AAGTGTAACT TACATGCACT GGTACCAGCA GAAGCCAGGT 120

AAGGCTCCAA AGCTGCTGAT CTACAGCACA TCCAACCTGG CTTCTGGTGT GCCAAGCAGA 180

TTCTCCGGAA GCGGTAGCGG CACCGACTAC ACCTTCACCA TCAGCAGCCT CCAGCCAGAG 240

GATATCGCCA CCTACTACTG CCAGCAGAGG AGTACTTACC CGCTCACGTT CGGCCAAGGG 300

ACCAAGCTCG AGATCAAACG G 321

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GGCCAGATCG TGCTGACCCA GAGCCCAAGC AGCCTGAGCG 40

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

CTAGCGCTCA GGCTGCTTGG GCTCTGGGTC AGCACGATCT GGCCGC 46

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

CAGATCGTGC TGACCCAGAG CCCAAGCAGC CTGAGCGCTA GCGTGGGTGA CAGAGTGACC 60

ATCACGTGTA GTGCCAGCTC AAGTGTAACT TACATGCACT GGTACCAGCA GAAGCCAGGT 120

AAGGCTCCAA AGCTGCTGAT CTACAGCACA TCCAACCTGG CTTCTGGTGT GCCAAGCAGA 180

TTCTCCGGAA GCGGTAGCGG CACCGACTAC ACCTTCACCA TCAGCAGCCT CCAGCCAGAG 240

GATATCGCCA CCTACTACTG CCAGCAGAGG AGTACTTACC CGCTCACGTT CGGCCAAGGG 300

ACCAAGCTCG AGATCAAACG G 321

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Gln Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

CGTATTAGTC ATCGCTATTA CC 22

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GTTGGATGTG CTGTAGATCC ACAGCTTTGG AGCCTTACC 39

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

TCCGTTTGAT CTCGAGCTTG G 21

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GGTAAGGCTC CAAAGCTGTG GATCTACAGC ACATCCAAC 39

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GACATCCAGA TGACCCAGAG CCCAAGCAGC CTGAGCGCTA GCGTGGGTGA CAGAGTGACC 60

ATCACGTGTA GTGCCAGCTC AAGTGTAACT TACATGCACT GGTACCAGCA GAAGCCAGGT 120

AAGGCTCCAA AGCTGTGGAT CTACAGCACA TCCAACCTGG CTTCTGGTGT GCCAAGCAGA 180

TTCTCCGGAA GCGGTAGCGG CACCGACTAC ACCTTCACCA TCAGCAGCCT CCAGCCAGAG 240

GATATCGCCA CCTACTACTG CCAGCAGAGG AGTACTTACC CGCTCACGTT CGGCCAAGGG 300

ACCAAGCTCG AGATCAAACG G 321

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

CCTTGAGTGG ATTGCATGGA TTGACCCTGA GAATGGTGAC ACTGAGTACG CACCTAAGTT 60

TCGC 64

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

GGCCGCGAAA CTTAGGTGCG TACTCAGTGT CACCATTCTC AGGGTCAATC CATGCAATCC 60

ACTCAAGG 68

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60

ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

CCTGGACGAG GCCTTGAGTG GATTGCATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180

GCACCTAAGT TTCGCGGCCG CGTGACAATG CTGGCAGACA CTAGTAAGAA CCAGTTCAGC 240

CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn
20 25 30

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

GGCCGCGTGA CAATGCTGGC AGACTCAAGT AAGAACCAGG CCAGCCTGAG ACTCAGCAGC 60

GTGACAGCCG CCGACACCGC 80

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GGTGTCGGCG GCTGTCACGC TGCTGAGTCT CAGGCTGGCC TGGTTCTTAC TTGAGTCTGC 60

CAGCATTGTC ACGC 74

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60

ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

CCTGGACGAG GCCTTGAGTG GATTGGATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180

GCACCTAAGT TTCGCGGCCG CGTGACAATG CTGGCAGACT CAAGTAAGAA CCAGGCCAGC 240

CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn
20 25 30

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Leu Ala Asp Ser Ser Lys Asn Gln Ala Ser
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60

ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

CCTGGACGAG GCCTTGAGTG GATTGCATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180

GCACCTAAGT TTCGCGGCCG CGTGACAATG CTGGCAGACT CAAGTAAGAA CCAGGCCAGC 240

CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn
20 25 30

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Leu Ala Asp Ser Ser Lys Asn Gln Ala Ser
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

GGCCGCGCCA CAATGCTGGC AGACACTAGT AAGAACCAGT TCAGCCTGAG ACTCAGCAGC 60

GTGACAGCCG CCGACACCGC 80

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

GGTGTCGGCG GCTGTCACGC TGCTGAGTCT CAGGCTGAAC TGGTTCTTAC TAGTGTCTGC 60

CAGCATTGTG GCGC 74

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60

ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

CCTGGACGAG GCCTTGAGTG GATTGGATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180

GCACCTAAGT TTCGCGGCCG CGCCACAATG CTGGCAGACA CTAGTAAGAA CCAGTTCAGC 240

CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn
20 25 30

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Arg Gly Arg Ala Thr Met Leu Ala Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

GGCCGCGCCA CAATGCTGGC AGACTCAAGT AAGAACCAGG CCAGCCTGAG ACTCAGCAGC 60

GTGACAGCCG CCGACACCGC 80

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

GGTGTCGGCG GCTGTCACGC TGCTGAGTCT CAGGCTGGCC TGGTTCTTAC TTGAGTCTGC 60

CAGCATTGTG GCGC 74

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60

ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

CCTGGACGAG GCCTTGAGTG GATTGGATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180

GCACCTAAGT TTCGCGGCCG CGCCACAATG CTGGCAGACT CAAGTAAGAA CCAGGCCAGC 240

CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn
20 25 30

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Arg Gly Arg Ala Thr Met Leu Ala Asp Ser Ser Lys Asn Gln Ala Ser
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60

ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

CCTGGACGAG GCCTTGAGTG GATTGCATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180

GCACCTAAGT TTCGCGGCCG CGCCACAATG CTGGCAGACT CAAGTAAGAA CCAGGCCAGC 240

CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn
20 25 30

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Arg Gly Arg Ala Thr Met Leu Ala Asp Ser Ser Lys Asn Gln Ala Ser
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 780 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

ATGAAGTTGT GGCTGAACTG GATTTTCCTT GTAACACTTT TAAATGGAAT TCAGTGTGAG 60

GTGCAGCTGC AGCAGAGCGG TCCAGGTCTC GTACGGCCTA GCCAGACCCT GAGCCTCACG 120

TGCACCGCAT CTGGCTTCAA CATTAAGGAC AATTACATGC ACTGGGTGAG ACAGCCACCT 180

GGACGAGGCC TTGAGTGGAT TGGATGGATT GACCCTGAGA ATGGTGACAC TGAGTACGCA 240

CCTAAGTTTC GCGGCCGCGT GACAATGCTG GCAGACACTA GTAAGAACCA GTTCAGCCTG 300

AGACTCAGCA GCGTGACAGC CGCCGACACC GCGGTCTATT ATTGTCACGT CCTGATATAC 360

GCCGGGTATC TGGCAATGGA CTACTGGGGC CAAGGGACCC TCGTCACCGT GAGCTCGGCC 420

TCCACCAAGG GCCCATCGGT CTTCCCCCTG GCACCCTCCT CCAAGAGCAC CTCTGGGGGC 480

ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 540

AACTCAGGCG CCCTGACCAG CGGCGTGCAC ACCTTCCCGG CTGTCCTACA GTCCTCAGGA 600

CTCTACTCCC TCAGCAGCGT GGTGACTGTG CCCTCCAGCA GCTTGGGCAC CCAGACCTAC 660

ATCTGCAACG TGAATCACAA CCCCAGCAAC ACCAAGGTCG ACAAGAAAGT TGAGCCCAAA 720

TCTTGTGACA AGACGCACAC GTGCCCGCCG TGCCCGGCTC CGGAACTGCT GGGTGGCCCG 780

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly
1 5 10 15

Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg
20 25 30

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
35 40 45

Lys Asp Asn Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
50 55 60

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala
65 70 75 80

Pro Lys Phe Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn
85 90 95

Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
100 105 110

Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr
115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
195 200 205

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
210 215 220

Asn His Asn Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
225 230 235 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
245 250 255

Leu Gly Gly Pro
260

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 918 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

ATGAAGTTGT GGCTGAACTG GATTTTCCTT GTAACACTTT TAAATGGAAT TCAGTGTGAG 60

GTGCAGCTGC AGCAGAGCGG TCCAGGTCTC GTACGGCCTA GCCAGACCCT GAGCCTCACG 120

TGCACCGCAT CTGGCTTCAA CATTAAGGAC AATTACATGC ACTGGGTGAG ACAGCCACCT 180

GGACGAGGCC TTGAGTGGAT TGGATGGATT GACCCTGAGA ATGGTGACAC TGAGTACGCA 240

CCTAAGTTTC GCGGCCGCGT GACAATGCTG GCAGACACTA GTAAGAACCA GTTCAGCCTG 300

AGACTCAGCA GCGTGACAGC CGCCGACACC GCGGTCTATT ATTGTCACGT CCTGATATAC 360

GCCGGGTATC TGGCAATGGA CTACTGGGGC CAAGGGACCC TCGTCACCGT GAGCTCGGCT 420

AGCACCAAGG GCCCATCGGT CTTCCCCCTG GCGCCCTGCT CCAGGAGCAC CTCTGGGGGC 480

ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 540

AACTCAGGCG CCCTGACCAG CGGCGTGCAC ACCTTCCCGG CTGTCCTACA GTCCTCAGGA 600

CTCTACTCCC TCAGCAGCGT GGTGACCGTG CCCTCCAGCA GCTTGGGCAC CCAGACCTAC 660

ACCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGAGAGT GGAGCTGAAA 720

ACCCCACTCG GTGACACAAC TCACACGTGC CCTAGGTGTC CTGAACCTAA ATCTTGTGAC 780

ACACCTCCCC CGTGCCCACG GTGCCCAGAG CCCAAATCTT GCGACACGCC CCCACCGTGT 840

CCCAGATGTC CTGAACCAAA GAGCTGTGAC ACTCCACCGC CCTGCCCGAG GTGCCCAGCA 900

CCTGAACTCC TGGGAGGG 918

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly
1 5 10 15

Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg
20 25 30

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
35 40 45

Lys Asp Asn Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
50 55 60

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala
65 70 75 80

Pro Lys Phe Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn
85 90 95

Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
100 105 110

Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr
115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly
145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
195 200 205

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val
210 215 220

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Leu Lys
225 230 235 240

Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro Glu Pro
245 250 255

Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys
260 265 270

Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser
275 280 285

Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu
290 295 300

Gly Gly
305

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 705 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

ATGGATTTTC AAGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCTTCAGT CATAATGTCC 60

CGCGGCCAGA TCGTGCTGAC CCAGAGCCCA AGCAGCCTGA GCGCTAGCGT GGGTGACAGA 120

GTGACCATCA CGTGTAGTGC CAGCTCAAGT GTAACTTACA TGCACTGGTA CCAGCAGAAG 180

CCAGGTAAGG CTCCAAAGCT GCTGATCTAC AGCACATCCA ACCTGGCTTC TGGTGTGCCA 240

AGCAGATTCT CCGGAAGCGG TAGCGGCACC GACTACACCT TCACCATCAG CAGCCTCCAG 300

CCAGAGGATA TCGCCACCTA CTACTGCCAG CAGAGGAGTA CTTACCCGCT CACGTTCGGC 360

CAAGGGACCA AGCTCGAGAT CAAACGGACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 420

CCATCTGATG AGCAGTTGAA ATCTGGAACT GCCTCTGTTG TGTGCCTGCT GAATAACTTC 480

TATCCCAGAG AGGCCAAAGT ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 540

CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCCTG 600

ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 660

GGCCTGAGTT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGT 705

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser
35 40 45

Ser Ser Val Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
50 55 60

Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg
100 105 110

Ser Thr Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 705 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

ATGGATTTTC AAGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCTTCAGT CATAATGTCC 60

CGCGGCGACA TCCAGATGAC CCAGAGCCCA AGCAGCCTGA GCGCTAGCGT GGGTGACAGA 120

GTGACCATCA CGTGTAGTGC CAGCTCAAGT GTAACTTACA TGCACTGGTA CCAGCAGAAG 180

CCAGGTAAGG CTCCAAAGCT GTGGATCTAC AGCACATCCA ACCTGGCTTC TGGTGTGCCA 240

AGCAGATTCT CCGGAAGCGG TAGCGGCACC GACTACACCT TCACCATCAG CAGCCTCCAG 300

CCAGAGGATA TCGCCACCTA CTACTGCCAG CAGAGGAGTA CTTACCCGCT CACGTTCGGC 360

CAAGGGACCA AGCTCGAGAT CAAACGGACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 420

CCATCTGATG AGCAGTTGAA ATCTGGAACT GCCTCTGTTG TGTGCCTGCT GAATAACTTC 480

TATCCCAGAG AGGCCAAAGT ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 540

CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCCTG 600

ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 660

GGCCTGAGTT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGT 705

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser
35 40 45

Ser Ser Val Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
50 55 60

Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile
85 90 95

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg
100 105 110

Ser Thr Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

CCCAGCACCT GAACTCCTGG GAGGAGCAAC AGGACACAGT TATGAGAAGT ACAA 54

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

GGGGGTCTAG ATTATTAGTA CAGGTGTTCC AGGACGTAGC TGGCAACATA 50

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

GGGGGAGCTC GGCTAGCACC AAGGGCCCAT CGGTCTTCCC CCTGGC 46

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

TTGTACTTCT CATAACTGTG TCCTGTTGCT CCTCCCAGGA GTTCAGGTGC TGGGC 55

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

GCCTGTGCTC AATATTGATG G 21

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GGAGAAAGCC ATATCTGCCT G 21

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

TCGCTATTAC CATGGTGATG CGGTTTTGGC 30

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GGCTGGATTC TCAGTGGCGA CTT 23

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CACAACAGAG GCAGTTCC 18

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CACCTTCACC ATCAGCAGCC 20

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

GGACCTGCTG CAGAGTCTG 19

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

GGCTGCAGGA ATTCTTATTA TAGACGAACC CGGCTATCAA ACTGAGC 47

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1870 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

AAGCTTGCCG CCACCATGAA GTTGTGGCTG AACTGGATTT TCCTTGTAAC ACTTTTAAAT 60

GGAATTCAGT GTGAGGTGCA GCTGCAGCAG AGCGGTCCAG GTCTCGTACG GCCTAGCCAG 120

ACCCTGAGCC TCACGTGCAC CGCATCTGGC TTCAACATTA AGGACAATTA CATGCACTGG 180

GTGAGACAGC CACCTGGACG AGGCCTTGAG TGGATTGGAT GGATTGACCC TGAGAATGGT 240

GACACTGAGT ACGCACCTAA GTTTCGCGGC CGCGTGACAA TGCTGGCAGA CACTAGTAAG 300

AACCAGTTCA GCCTGAGACT CAGCAGCGTG ACAGCCGCCG ACACCGCGGT CTATTATTGT 360

CACGTCCTGA TATACGCCGG GTATCTGGCA ATGGACTACT GGGGCCAAGG GACCCTCGTC 420

ACCGTGAGCT CGGCTAGCAC CAAGGGCCCA TCGGTCTTCC CCCTGGCGCC CTGCTCCAGG 480

AGCACCTCTG GGGGCACAGC GGCCCTGGGC TGCCTGGTCA AGGACTACTT CCCCGAACCG 540

GTGACGGTGT CGTGGAACTC AGGCGCCCTG ACCAGCGGCG TGCACACCTT CCCGGCTGTC 600

CTACAGTCCT CAGGACTCTA CTCCCTCAGC AGCGTGGTGA CCGTGCCCTC CAGCAGCTTG 660

GGCACCCAGA CCTACACCTG CAACGTGAAT CACAAGCCCA GCAACACCAA GGTGGACAAG 720

AGAGTGGAGC TGAAAACCCC ACTCGGTGAC ACAACTCACA CGTGCCCTAG GTGTCCTGAA 780

CCTAAATCTT GTGACACACC TCCCCCGTGC CCACGGTGCC CAGAGCCCAA ATCTTGCGAC 840

ACGCCCCCAC CGTGTCCCAG ATGTCCTGAA CCAAAGAGCT GTGACACTCC ACCGCCCTGC 900

CCGAGGTGCC CAGCACCTGA ACTCCTGGGA GGAGCAACAG GACACAGTTA TGAGAAGTAC 960

AACAAGTGGG AAACGATAGA GGCTTGGACT CAACAAGTCG CCACTGAGAA TCCAGCCCTC 1020

ATCTCTCGCA GTGTTATCGG AACCACATTT GAGGGACGCG CTATTTACCT CCTGAAGGTT 1080

GGCAAAGCTG GACAAAATAA GCCTGCCATT TTCATGGACT GTGGTTTCCA TGCCAGAGAG 1140

TGGATTTCTC CTGCATTCTG CCAGTGGTTT GTAAGAGAGG CTGTTCGTAC CTATGGACGT 1200

GAGATCCAAG TGACAGAGCT TCTCGACAAG TTAGACTTTT ATGTCCTGCC TGTGCTCAAT 1260

ATTGATGGCT ACATCTACAC CTGGACCAAG AGCCGATTTT GGAGAAAGAC TCGCTCCACC 1320

CATACTGGAT CTAGCTGCAT TGGCACAGAC CCCAACAGAA ATTTTGATGC TGGTTGGTGT 1380

GAAATTGGAG CCTCTCGAAA CCCCTGTGAT GAAACTTACT GTGGACCTGC CGCAGAGTCT 1440

GAAAAGGAGA CCAAGGCCCT GGCTGATTTC ATCCGCAACA AACTCTCTTC CATCAAGGCA 1500

TATCTGACAA TCCACTCGTA CTCCCAAATG ATGATCTACC CTTACTCATA TGCTTACAAA 1560

CTCGGTGAGA ACAATGCTGA GTTGAATGCC CTGGCTAAAG CTACTGTGAA AGAACTTGCC 1620

TCACTGCACG GCACCAAGTA CACATATGGC CCGGGAGCTA CAACAATCTA TCCTTCTGCT 1680

GGGACTTCTA AAGACTGGGC TTATGACCAA GGAATCAGAT ATTCCTTCAC CTTTGAACTT 1740

CGAGATACAG GCAGATATGG CTTTCTCCTT CCAGAATCCC AGATCCGGGC TACCTGCGAG 1800

GAGACCTTCC TGGCAATCAA GTATGTTGCC AGCTACGTCC TGGAACACCT GTACTAATAA 1860

TCTAGAGAGA 1870

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 613 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly
1 5 10 15

Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg
20 25 30

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
35 40 45

Lys Asp Asn Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
50 55 60

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala
65 70 75 80

Pro Lys Phe Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn
85 90 95

Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
100 105 110

Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr
115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly
145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
195 200 205

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val
210 215 220

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Leu Lys
225 230 235 240

Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro Glu Pro
245 250 255

Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys
260 265 270

Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser
275 280 285

Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu
290 295 300

Gly Gly Ala Thr Gly His Ser Tyr Glu Lys Tyr Asn Lys Trp Glu Thr
305 310 315 320

Ile Glu Ala Trp Thr Gln Gln Val Ala Thr Glu Asn Pro Ala Leu Ile
325 330 335

Ser Arg Ser Val Ile Gly Thr Thr Phe Glu Gly Arg Ala Ile Tyr Leu
340 345 350

Leu Lys Val Gly Lys Ala Gly Gln Asn Lys Pro Ala Ile Phe Met Asp
355 360 365

Cys Gly Phe His Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Gln Trp
370 375 380

Phe Val Arg Glu Ala Val Arg Thr Tyr Gly Arg Glu Ile Gln Val Thr
385 390 395 400

Glu Leu Leu Asp Lys Leu Asp Phe Tyr Val Leu Pro Val Leu Asn Ile
405 410 415

Asp Gly Tyr Ile Tyr Thr Trp Thr Lys Ser Arg Phe Trp Arg Lys Thr
420 425 430

Arg Ser Thr His Thr Gly Ser Ser Cys Ile Gly Thr Asp Pro Asn Arg
435 440 445

Asn Phe Asp Ala Gly Trp Cys Glu Ile Gly Ala Ser Arg Asn Pro Cys
450 455 460

Asp Glu Thr Tyr Cys Gly Pro Ala Ala Glu Ser Glu Lys Glu Thr Lys
465 470 475 480

Ala Leu Ala Asp Phe Ile Arg Asn Lys Leu Ser Ser Ile Lys Ala Tyr
485 490 495

Leu Thr Ile His Ser Tyr Ser Gln Met Met Ile Tyr Pro Tyr Ser Tyr
500 505 510

Ala Tyr Lys Leu Gly Glu Asn Asn Ala Glu Leu Asn Ala Leu Ala Lys
515 520 525

Ala Thr Val Lys Glu Leu Ala Ser Leu His Gly Thr Lys Tyr Thr Tyr
530 535 540

Gly Pro Gly Ala Thr Thr Ile Tyr Pro Ser Ala Gly Thr Ser Lys Asp
545 550 555 560

Trp Ala Tyr Asp Gln Gly Ile Arg Tyr Ser Phe Thr Phe Glu Leu Arg
565 570 575

Asp Thr Gly Arg Tyr Gly Phe Leu Leu Pro Glu Ser Gln Ile Arg Ala
580 585 590

Thr Cys Glu Glu Thr Phe Leu Ala Ile Lys Tyr Val Ala Ser Tyr Val
595 600 605

Leu Glu His Leu Tyr
610

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 96 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

His His Gly Gly Glu His Phe Glu Gly Glu Lys Val Phe Arg Val Asn
1 5 10 15

Val Glu Asp Glu Asn His Ile Asn Ile Ile Arg Glu Leu Ala Ser Thr
20 25 30

Thr Gln Ile Asp Phe Trp Lys Pro Asp Ser Val Thr Gln Ile Lys Pro
35 40 45

His Ser Thr Val Asp Phe Arg Val Lys Ala Glu Asp Thr Val Thr Val
50 55 60

Glu Asn Val Leu Lys Gln Asn Glu Leu Gln Tyr Lys Val Leu Ile Ser
65 70 75 80

Asn Leu Arg Asn Val Val Glu Ala Gln Phe Asp Ser Arg Val Arg Leu
85 90 95

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 520 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GAGCTCGGCT AGCACCAAGG GCCCATCGGT CTTCCCCCTG GCGCCCTGCT CCAGGAGCAC 60

CTCTGGGGGC ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC 120

GGTGTCGTGG AACTCAGGCG CCCTGACCAG CGGCGTGCAC ACCTTCCCGG CTGTCCTACA 180

GTCCTCAGGA CTCTACTCCC TCAGCAGCGT GGTGACCGTG CCCTCCAGCA GCTTGGGCAC 240

CCAGACCTAC ACCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGAGAGT 300

GGAGCTGAAA ACCCCACTCG GTGACACAAC TCACACGTGC CCTAGGTGTC CTGAACCTAA 360

ATCTTGTGAC ACACCTCCCC CGTGCCCACG GTGCCCAGAG CCCAAATCTT GCGACACGCC 420

CCCACCGTGT CCCAGATGTC CTGAACCAAA GAGCTGTGAC ACTCCACCGC CCTGCCCGAG 480

GTGCCCAGCA CCTGAACTCC TGGGAGGGTA ATAGCCCGGG 520

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

GTTATTACTC GCTGCCCAAC CAGCCATGGC G 31

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

GCAGCAGGAT AGATTGTTGT AGC 23

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

CCGGAATTCT TATTAGTTCA GGTCCTCCTC AGAGATCAGC TTCTGCTCCT CGAACTCATG 60

GTGGTGATGG TGGTGGTACA GGTGTTCC 88

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

CAATCTATCC TGCTGCTGGG ACTTCTAAAG 30

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

GATTGTTGTA GCTCCCGGGC 20

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

GGAGCTACAA CAATCTATCC TTCTGCTGGG 30

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

ACGGCACCAA GTACACATAT GG 22

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

ACGAGAATTC GACCGCTCTG CTGCAGCTGC ACCTCGGAAC CGCCACCGCT GCCACCGCCA 60

GAACCGCCAC CGTACAGGTG TTCCAGGACG 90

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2154 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

ATGTTGGCAC TCTTGGTTCT GGTGACTGTG GCCCTGGCAT CTGCTCATCA TGGTGGTGAG 60

CACTTTGAAG GCGAGAAGGT GTTCCGTGTT AACGTTGAAG ATGAAAATCA CATTAACATA 120

ATCCGCGAGT TGGCCAGCAC GACCCAGATT GACTTCTGGA AGCCAGATTC TGTCACACAA 180

ATCAAACCTC ACAGTACAGT TGACTTCCGT GTTAAAGCAG AAGATACTGT CACTGTGGAG 240

AATGTTCTAA AGCAGAATGA ACTACAATAC AAGGTACTGA TAAGCAACCT GAGAAATGTG 300

GTGGAGGCTC AGTTTGATAG CCGGGTTCGT GCAACAGGAC ACAGTTATGA GAAGTACAAC 360

AAGTGGGAAA CGATAGAGGC TTGGACTCAA CAAGTCGCCA CTGAGAATCC AGCCCTCATC 420

TCTCGCAGTG TTATCGGAAC CACATTTGAG GGACGCGCTA TTTACCTCCT GAAGGTTGGC 480

AAAGCTGGAC AAAATAAGCC TGCCATTTTC ATGGACTGTG GTTTCCATGC CAGAGAGTGG 540

ATTTCTCCTG CATTCTGCCA GTGGTTTGTA AGAGAGGCTG TTCGTACCTA TGGACGTGAG 600

ATCCAAGTGA CAGAGCTTCT CGACAAGTTA GACTTTTATG TCCTGCCTGT GCTCAATATT 660

GATGGCTACA TCTACACCTG GACCAAGAGC CGATTTTGGA GAAAGACTCG CTCCACCCAT 720

ACTGGATCTA GCTGCATTGG CACAGACCCC AACAGAAATT TTGATGCTGG TTGGTGTGAA 780

ATTGGAGCCT CTCGAAACCC CTGTGATGAA ACTTACTGTG GACCTGCCGC AGAGTCTGAA 840

AAGGAGACCA AGGCCCTGGC TGATTTCATC CGCAACAAAC TCTCTTCCAT CAAGGCATAT 900

CTGACAATCC ACTCGTACTC CCAAATGATG ATCTACCCTT ACTCATATGC TTACAAACTC 960

GGTGAGAACA ATGCTGAGTT GAATGCCCTG GCTAAAGCTA CTGTGAAAGA ACTTGCCTCA 1020

CTGCACGGCA CCAAGTACAC ATATGGCCCG GGAGCTACAA CAATCTATCC TTCTGCTGGG 1080

ACTTCTAAAG ACTGGGCTTA TGACCAAGGA ATCAGATATT CCTTCACCTT TGAACTTCGA 1140

GATACAGGCA GATATGGCTT TCTCCTTCCA GAATCCCAGA TCCGGGCTAC CTGCGAGGAG 1200

ACCTTCCTGG CAATCAAGTA TGTTGCCAGC TACGTCCTGG AACACCTGTA CGGTGGCGGT 1260

TCTGGCGGTG GCAGCGGTGG CGGTTCCGAG GTGCAGCTGC AGCAGAGCGG TCCAGGTCTC 1320

GTACGGCCTA GCCAGACCCT GAGCCTCACG TGCACCGCAT CTGGCTTCAA CATTAAGGAC 1380

AATTACATGC ACTGGGTGAG ACAGCCACCT GGACGAGGCC TTGAGTGGAT TGGATGGATT 1440

GACCCTGAGA ATGGTGACAC TGAGTACGCA CCTAAGTTTC GCGGCCGCGT GACAATGCTG 1500

GCAGACACTA GTAAGAACCA GTTCAGCCTG AGACTCAGCA GCGTGACAGC CGCCGACACC 1560

GCGGTCTATT ATTGTCACGT CCTGATATAC GCCGGGTATC TGGCAATGGA CTACTGGGGC 1620

CAAGGGACCC TCGTCACCGT GAGCTCGGCT AGCACCAAGG GCCCATCGGT CTTCCCCCTG 1680

GCGCCCTGCT CCAGGAGCAC CTCTGGGGGC ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC 1740

TACTTCCCCG AACCGGTGAC GGTGTCGTGG AACTCAGGCG CCCTGACCAG CGGCGTGCAC 1800

ACCTTCCCGG CTGTCCTACA GTCCTCAGGA CTCTACTCCC TCAGCAGCGT GGTGACCGTG 1860

CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ACCTGCAACG TGAATCACAA GCCCAGCAAC 1920

ACCAAGGTGG ACAAGAGAGT GGAGCTGAAA ACCCCACTCG GTGACACAAC TCACACGTGC 1980

CCTAGGTGTC CTGAACCTAA ATCTTGTGAC ACACCTCCCC CGTGCCCACG GTGCCCAGAG 2040

CCCAAATCTT GCGACACGCC CCCACCGTGT CCCAGATGTC CTGAACCAAA GAGCTGTGAC 2100

ACTCCACCGC CCTGCCCGAG GTGCCCAGCA CCTGAACTCC TGGGAGGGTA ATAG 2154

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 716 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

Met Leu Ala Leu Leu Val Leu Val Thr Val Ala Leu Ala Ser Ala His
1 5 10 15

His Gly Gly Glu His Phe Glu Gly Glu Lys Val Phe Arg Val Asn Val
20 25 30

Glu Asp Glu Asn His Ile Asn Ile Ile Arg Glu Leu Ala Ser Thr Thr
35 40 45

Gln Ile Asp Phe Trp Lys Pro Asp Ser Val Thr Gln Ile Lys Pro His
50 55 60

Ser Thr Val Asp Phe Arg Val Lys Ala Glu Asp Thr Val Thr Val Glu
65 70 75 80

Asn Val Leu Lys Gln Asn Glu Leu Gln Tyr Lys Val Leu Ile Ser Asn
85 90 95

Leu Arg Asn Val Val Glu Ala Gln Phe Asp Ser Arg Val Arg Ala Thr
100 105 110

Gly His Ser Tyr Glu Lys Tyr Asn Lys Trp Glu Thr Ile Glu Ala Trp
115 120 125

Thr Gln Gln Val Ala Thr Glu Asn Pro Ala Leu Ile Ser Arg Ser Val
130 135 140

Ile Gly Thr Thr Phe Glu Gly Arg Ala Ile Tyr Leu Leu Lys Val Gly
145 150 155 160

Lys Ala Gly Gln Asn Lys Pro Ala Ile Phe Met Asp Cys Gly Phe His
165 170 175

Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Gln Trp Phe Val Arg Glu
180 185 190

Ala Val Arg Thr Tyr Gly Arg Glu Ile Gln Val Thr Glu Leu Leu Asp
195 200 205

Lys Leu Asp Phe Tyr Val Leu Pro Val Leu Asn Ile Asp Gly Tyr Ile
210 215 220

Tyr Thr Trp Thr Lys Ser Arg Phe Trp Arg Lys Thr Arg Ser Thr His
225 230 235 240

Thr Gly Ser Ser Cys Ile Gly Thr Asp Pro Asn Arg Asn Phe Asp Ala
245 250 255

Gly Trp Cys Glu Ile Gly Ala Ser Arg Asn Pro Cys Asp Glu Thr Tyr
260 265 270

Cys Gly Pro Ala Ala Glu Ser Glu Lys Glu Thr Lys Ala Leu Ala Asp
275 280 285

Phe Ile Arg Asn Lys Leu Ser Ser Ile Lys Ala Tyr Leu Thr Ile His
290 295 300

Ser Tyr Ser Gln Met Met Ile Tyr Pro Tyr Ser Tyr Ala Tyr Lys Leu
305 310 315 320

Gly Glu Asn Asn Ala Glu Leu Asn Ala Leu Ala Lys Ala Thr Val Lys
325 330 335

Glu Leu Ala Ser Leu His Gly Thr Lys Tyr Thr Tyr Gly Pro Gly Ala
340 345 350

Thr Thr Ile Tyr Pro Ser Ala Gly Thr Ser Lys Asp Trp Ala Tyr Asp
355 360 365

Gln Gly Ile Arg Tyr Ser Phe Thr Phe Glu Leu Arg Asp Thr Gly Arg
370 375 380

Tyr Gly Phe Leu Leu Pro Glu Ser Gln Ile Arg Ala Thr Cys Glu Glu
385 390 395 400

Thr Phe Leu Ala Ile Lys Tyr Val Ala Ser Tyr Val Leu Glu His Leu
405 410 415

Tyr Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
420 425 430

Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln Thr Leu Ser
435 440 445

Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn Tyr Met His
450 455 460

Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly Trp Ile
465 470 475 480

Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe Arg Gly Arg
485 490 495

Val Thr Met Leu Ala Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg Leu
500 505 510

Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys His Val Leu
515 520 525

Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
530 535 540

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
545 550 555 560

Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
565 570 575

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
580 585 590

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
595 600 605

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
610 615 620

Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn
625 630 635 640

Thr Lys Val Asp Lys Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr
645 650 655

Thr His Thr Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro
660 665 670

Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro
675 680 685

Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro
690 695 700

Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu Gly Gly
705 710 715

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

TATATAAAGC TTGCCGCCAC CATGGGCCAC ACACGGAGGC AG 42

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

ACTCCACCAG CTTCACCTCG TTATCAGGAA AATGCTCTTG CTTGG 45

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

AGAGCATTTT CCTGATAACG AGGTGAAGCT GGTGGAGTCT GGAGG 45

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

CCAGGCATCC CAGGGTCACC ATGGAGTTAG TTTGGGCAGC 40

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1446 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:16..1435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

```
AAGCTTGCCG CCACC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC        51
                 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser
                   1               5                  10

AAG TGT CCA TAC CTC AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT        99
Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu
          15                  20                  25

TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA       147
Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu
      30                  35                  40

GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG GCA       195
Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala
  45                  50                  55                  60

CAA ACT CGC ATC TAC TGG CAA AAG GAG AAG AAA ATG GTG CTG ACT ATG       243
Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met
                  65                  70                  75

ATG TCT GGG GAC ATG AAT ATA TGG CCC GAG TAC AAG AAC CGG ACC ATC       291
Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile
              80                  85                  90

TTT GAT ATC ACT AAT AAC CTC TCC ATT GTG ATC CTG GCT CTG CGC CCA       339
Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro
          95                  100                 105

TCT GAC GAG GGC ACA TAC GAG TGT GTT GTT CTG AAG TAT GAA AAA GAC       387
Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp
      110                 115                 120

GCT TTC AAG CGG GAA CAC CTG GCT GAA GTG ACG TTA TCA GTC AAA GCT       435
Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala
  125                 130                 135                 140
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GAC TTC CCT ACA CCT AGT ATA TCT GAC TTT GAA ATT CCA ACT TCT AAT      483
Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn
                145                 150                 155

ATT AGA AGG ATA ATT TGC TCA ACC TCT GGA GGT TTT CCA GAG CCT CAC      531
Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His
            160                 165                 170

CTC TCC TGG TTG GAA AAT GGA GAA GAA TTA AAT GCC ATC AAC ACA ACA      579
Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr
        175                 180                 185

GTT TCC CAA GAT CCT GAA ACT GAG CTC TAT GCT GTT AGC AGC AAA CTG      627
Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu
    190                 195                 200

GAT TTC AAT ATG ACA ACC AAC CAC AGC TTC ATG TGT CTC ATC AAG TAT      675
Asp Phe Asn Met Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr
205                 210                 215                 220

GGA CAT TTA AGA GTG AAT CAG ACC TTC AAC TGG AAT ACA ACC AAG CAA      723
Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln
                225                 230                 235

GAG CAT TTT CCT GAT AAC GAG GTG AAG CTG GTG GAG TCT GGA GGA GGC      771
Glu His Phe Pro Asp Asn Glu Val Lys Leu Val Glu Ser Gly Gly Gly
            240                 245                 250

TTG GTA CAG CCT GGG GGT TCT CTG AGA CTC TCC TGT GCA ACT TCT GGG      819
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly
        255                 260                 265

TTC ACC TTC ACT GAT TAC TAC ATG AAC TGG GTC CGC CAG CCT CCA GGA      867
Phe Thr Phe Thr Asp Tyr Tyr Met Asn Trp Val Arg Gln Pro Pro Gly
    270                 275                 280

AAG GCA CTT GAG TGG TTG GGT TTT ATT GGA AAC AAA GCT AAT GGT TAC      915
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Lys Ala Leu Glu Trp Leu Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr
285                 290                 295                 300

ACA ACA GAG TAC AGT GCA TCT GTG AAG GGT CGG TTC ACC ATC TCC AGA      963
Thr Thr Glu Tyr Ser Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
                305                 310                 315

GAC AAA TCC CAA AGC ATC CTC TAT CTT CAA ATG AAC ACC CTG AGA GCT     1011
Asp Lys Ser Gln Ser Ile Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala
            320                 325                 330

GAG GAC AGT GCC ACT TAT TAC TGT ACA AGA GAT AGG GGG CTA CGG TTC     1059
Glu Asp Ser Ala Thr Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe
        335                 340                 345

TAC TTT GAC TAC TGG GGC CAA GGC ACC ACT CTC ACA GTC TCC TCA GCC     1107
Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala
    350                 355                 360

AAA ACG ACA CCC CCA TCT GTC TAT CCA CTG GCC CCT GGA TCT GCT GCC     1155
Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala
365                 370                 375                 380

CAA ACT AAC TCC ATG GTG ACC CTG GGA TGC CTG GTC AAG GGC TAT TTC     1203
Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe
                385                 390                 395

CCT GAG CCA GTG ACA GTG ACC TGG AAC TCT GGA TCT CTG TCC AGC GGT     1251
Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
            400                 405                 410

GTG CAC ACC TTC CCA GCT GTC CTG CAG TCT GAC CTC TAC ACT CTG AGC     1299
Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
        415                 420                 425

AGC TCA GTG ACT GTC CCC TCC AGC ACC TGG CCC AGC GAG ACC GTC ACC     1347
Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
    430                 435                 440
```

```
TGC AAC GTT GCC CAC CCG GCC AGC AGC ACC AAG GTG GAC AAG AAA ATT      1395
Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
445                 450                 455                 460

GTG CCC AGG GAT TGT GGT TGT AAG CCT TGC ATA TGT ACA T AGTAAGAATT     1445
Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr
                465                 470

c                                                                    1446
```

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

```
Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
 1               5                  10                  15

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
            20                  25                  30

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
        35                  40                  45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
    50                  55                  60

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
65                  70                  75                  80
```

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
85 90 95

Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
100 105 110

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
115 120 125

Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
130 135 140

Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
145 150 155 160

Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
165 170 175

Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
180 185 190

Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
195 200 205

Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
210 215 220

Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
225 230 235 240

Asp Asn Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
245 250 255

Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Thr
260 265 270

Asp Tyr Tyr Met Asn Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu
275 280 285

Trp Leu Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr
290 295 300

Ser Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Gln
305 310 315 320

Ser Ile Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Ser Ala
325 330 335

Thr Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr
340 345 350

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro
355 360 365

Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
370 375 380

Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val
385 390 395 400

Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe
405 410 415

Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
420 425 430

Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
435 440 445

His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
450 455 460

Cys Gly Cys Lys Pro Cys Ile Cys Thr
465 470

CLAIMS

1. An anti-CEA antibody ("806.077 Ab") comprising complementarity determining regions (CDRs) in which the CDRs comprise the following sequences:

a) heavy chain

CDR1 DNYMH (SEQ ID NO: 29)

CDR2 WIDPENGDTE YAPKFRG (SEQ ID NO: 31)

CDR3 LIYAGYLAMD Y(SEQ ID NO: 32); and

b) light chain

CDR1 SASSSVTYMH (SEQ ID NO: 26)

CDR2 STSNLAS (SEQ ID NO: 27)

CDR3 QQRSTYPLT (SEQ ID NO: 28).

2. An antibody according to claim 1 in which the heavy chain CDRs 1 and 3 are further defined as:

CDR1 FNIKDNYMH (SEQ ID NO: 30); and

CDR3 HVLIYAGYLA MDY (SEQ ID NO: 33).

3. An antibody according to claim 1 comprising the following, optionally humanised, structure:

a heavy chain variable region sequence (SEQ ID NO: 11)

```
EVQLQQSGAE LVRSGASVKL SCTASGFNIK DNYMHWVKQR      40
PEQGLEWIAW IDPENGDTEY APKFRGKATL TADSSSNTAY      80
LHLSSLTSED TAVYYCHVLI YAGYLAMDYW GQGTSVAVSS      120
```

and;

a light chain variable region sequence (SEQ ID NO: 9):

```
DIELTQSPAI MSASPGEKVT ITCSASSSVT YMHWFQQKPG      40
TSPKLWIYST SNLASGVPAR FSGSGSGTSY SLTISRMEAE      80
DAATYYCQQR STYPLTFGAG TKLELKRA                   108.
```

4. A humanised antibody according to claim 3 comprising at least one of the following sequences:

a heavy chain variable region sequence which is VH1 (SEQ ID NO: 55);

a light chain variable region sequence which is VK4 (SEQ ID NO: 71);

a human CH1 heavy chain IgG3 constant region;

a human kappa light chain CL region; and

a human IgG3 hinge region;

optionally in the form of a $F(ab')_2$ fragment.

5. A conjugate comprising an antibody according to any preceding claim and an effector moiety.

6. A conjugate according to claim 5 in which the effector moiety is selected from any one of the following:

a) an enzyme suitable for use in an ADEPT system;

b) CPG2;

c) [G251T,D253K]HCPB;

d) [A248S,G251T,D253K]HCPB;

e) a co-stimulatory molecule;

f) extracellular domain of B7;

g) extracellular domain of human B7.1; and

h) extracellular domain of human B7.2;

optionally in the form of a fusion protein.

7. A conjugate according to claim 6 which is a fusion protein selected from any one of the following conjugates, (sequences being listed in N terminus to C terminus direction):

a) a humanised 806.077 $F(ab')_2$ - $\{[A248S,G251T,D253K]HCPB\}_2$ fusion comprising:

an antibody Fd' chain of structure VH1(SEQ ID NO: 55)/CH1 constant region from IgG3/hinge region from IgG3;

the Fd' chain being fused via its C terminus to the N terminus of [A248S,G251T,D253K]HCPB; and

an antibody light chain of formula VK4(SEQ ID NO: 71)/CL region from kappa light chain;

b) $\{[A248S,G251T,D253K]HCPB\}_2$-humanised 806.077 $F(ab')_2$ fusion comprising:

[A248S,G251T,D253K]HCPB;

the HCPB being fused at its C terminus, via a $(GGGS)_3$ linker, to the N terminus of an antibody Fd' chain of structure VH1(SEQ ID NO: 55)/CH1 constant region from IgG3/hinge region from IgG3; and

an antibody light chain of formula VK4(SEQ ID NO: 71)/CL region from kappa light chain; and

c) a (human B7.1 extracellular domain)$_2$ - humanised 806.077 F(ab')$_2$ fusion comprising:

human B7.1 extracellular domain;

the B7.1 being fused at its C terminus to the N terminus of an antibody Fd' chain of structure VH1(SEQ ID NO: 55)/CH1 constant region from IgG3/hinge region from IgG3; and

an antibody light chain of structure VK4(SEQ ID NO: 71)/CL region from kappa light chain.

8. A polynucleotide sequence capable of encoding a polypeptide of an antibody or a conjugate as defined in any preceding claim.

9. A vector comprising a polynucleotide as defined in claim 8.

10. A host cell transformed with a polynucleotide sequence as defined in claim 8 or a transgenic non-human animal or transgenic plant developed from the host cell.

11. Hybridoma 806.077 deposited as ECACC deposit no. 96022936.

12. A pharmaceutical composition comprising a conjugate as defined in any preceding claim in association with a pharmaceutically-acceptable diluent or carrier, optionally in a form suitable for intravenous administration.

13. A conjugate as described in any preceding claim for use as a medicament.

14. A method of making an antibody or a conjugate as defined in any preceding claim which comprises:

a) subjecting a host cell, a transgenic non-human mammal or a transgenic plant as defined in claim 10, or the hybridoma of claim 11, to conditions conducive to expression, and

optionally secretion, of the antibody or conjugate; and optionally

b) at least partially purifying the antibody or conjugate.

15. A method of treatment of a human or animal in need of such treatment which comprises administration to a human or animal of a pharmaceutically effective amount of a conjugate as defined in any preceding claim.

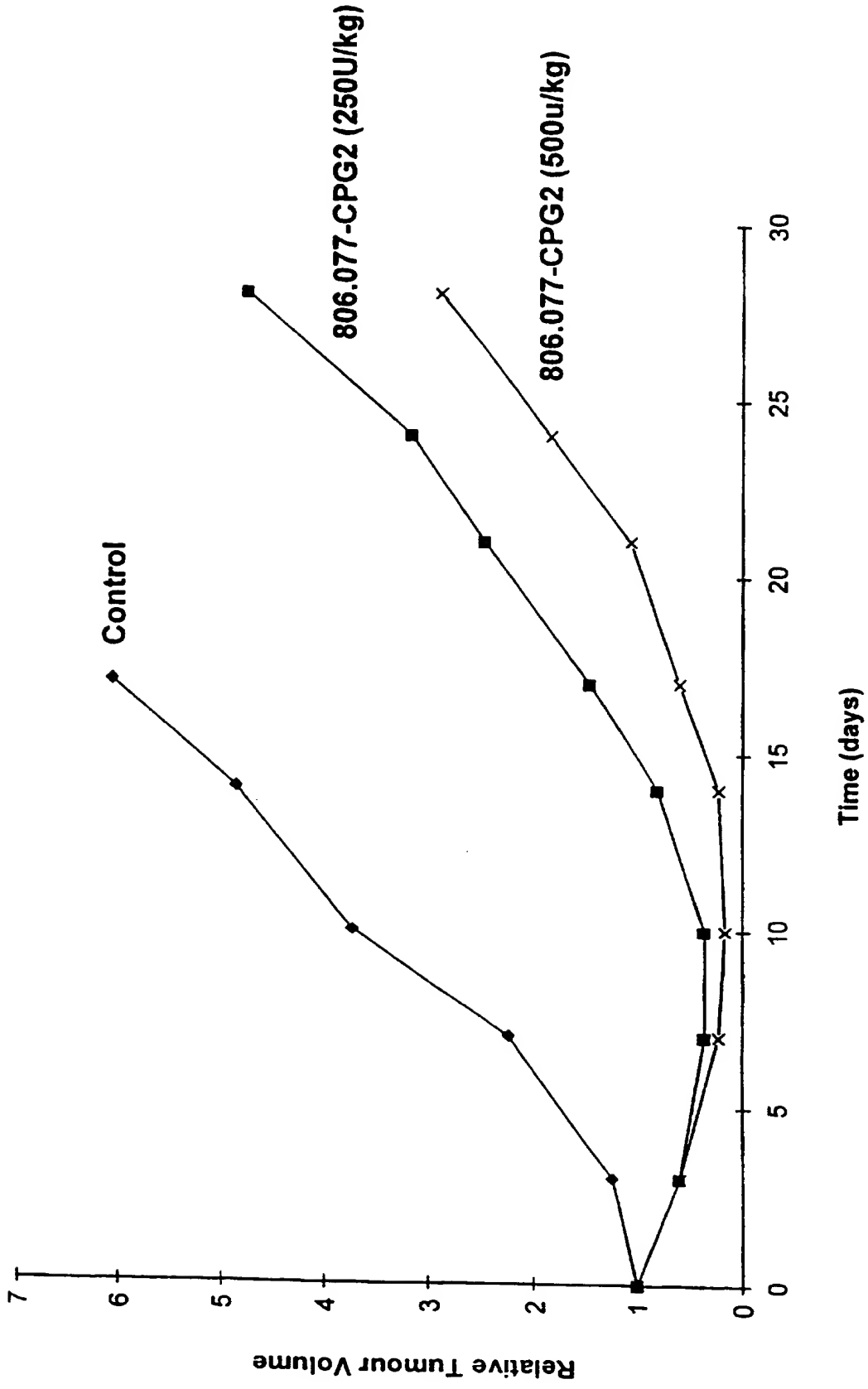
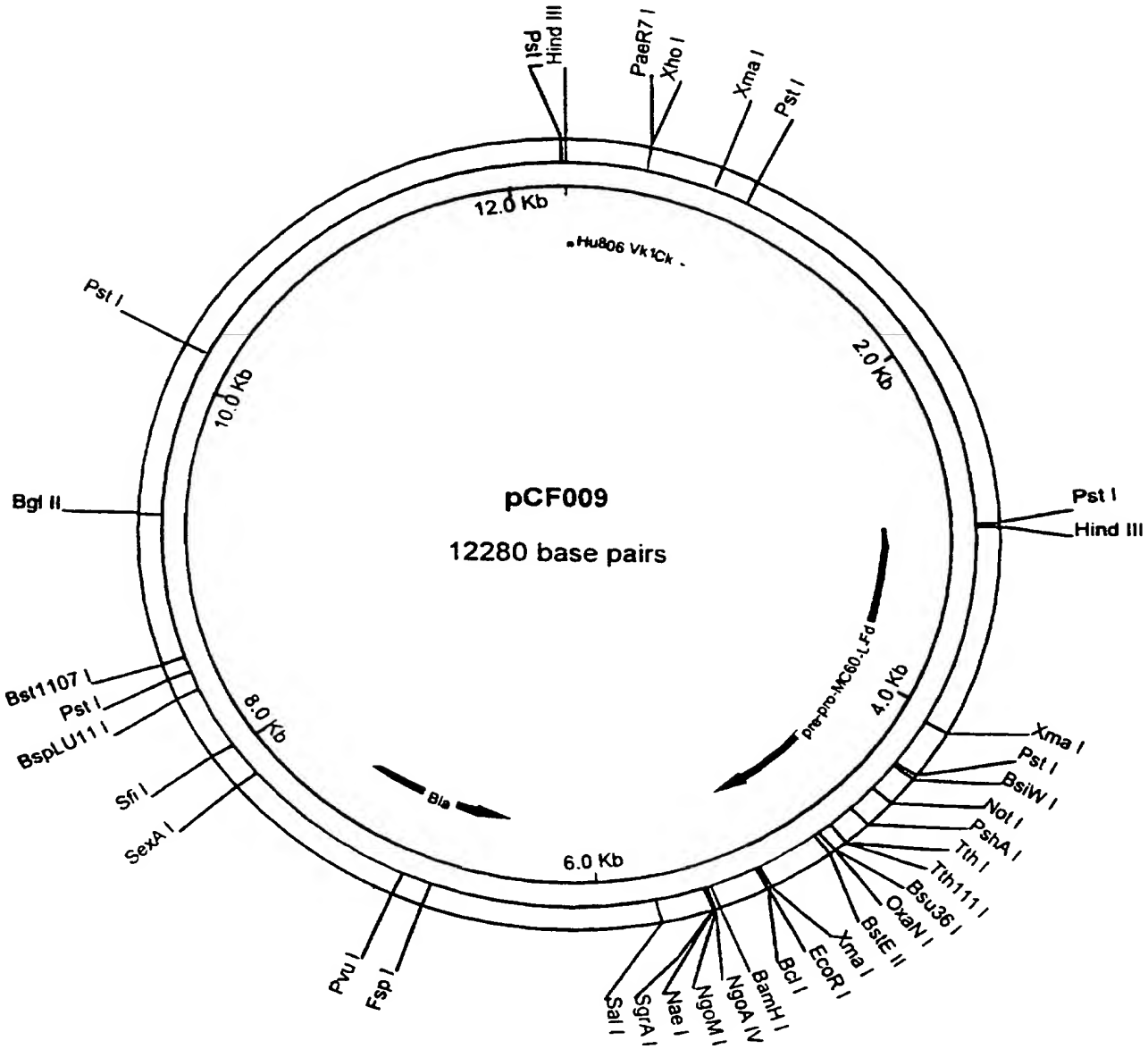


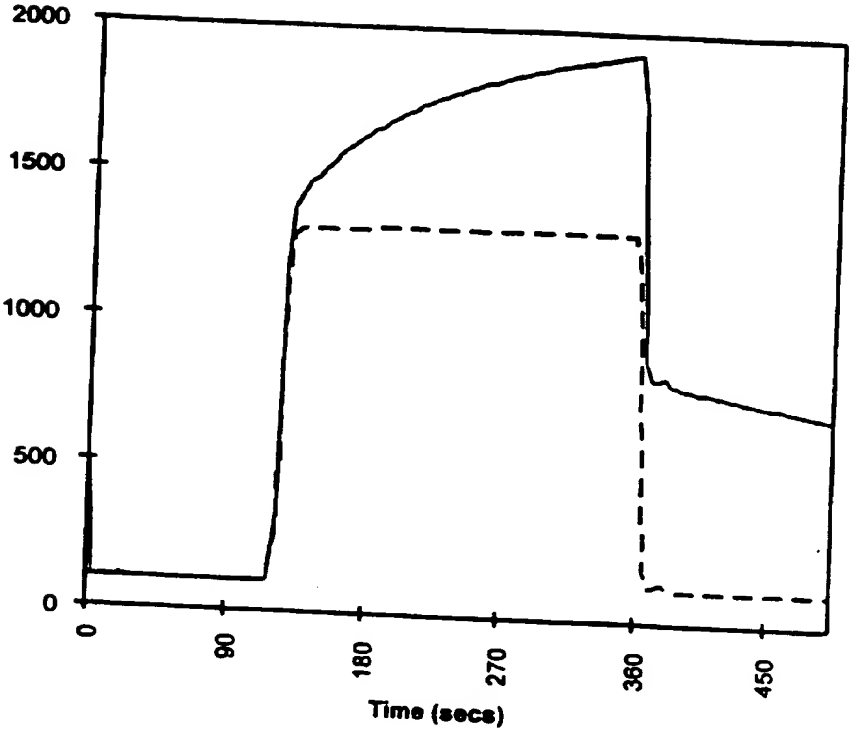
Figure 1

Figure 2



Single cut restriction enzymes
+ HindIII cuts twice
+ XmaI cuts three times
+ PstI cuts six times.

FIGURE 3



INTERNATIONAL SEARCH REPORT

Inter ..al Application No
PCT/GB 97/01165

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/62 C12N15/13 C07K16/30 C07K16/46 A61K47/48
C07K19/00 C07K14/705 C12N9/64 C12N5/10 C12N1/21
C12N5/20 //A01K67/027,A01H1/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP 0 633 029 A (CANCER RESEARCH CAMPAIGN TECHNOLOGY LTD.) 11 January 1995 see claims ---	1-6, 12-15
X	BRITISH JOURNAL OF CANCER, vol. 72, no. 5, November 1995, BASINGSTOKE, GB, pages 1083-1088, XP002038652 D. BLAKEY ET AL.: "Anti-tumour effects of an antibody-carboxypeptidase G2 conjugate in combination with phenol mustard prodrugs." see the whole document --- -/--	1-3,5,6, 12-15

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

1

Date of the actual completion of the international search	Date of mailing of the international search report
22 August 1997	04.09.97

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+ 31-70) 340-2040, Tx. 31 651 epo nl, Fax (+ 31-70) 340-3016	Nooij, F

Form PCT/ISA/210 (second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

Intern. ..al Application No
PCT/GB 97/01165

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 15341 A (CANCER RESEARCH CAMPAIGN TECHNOLOGY LTD.) 8 June 1995 see example 4 see figure 3 see seq. id. nos 1, 2	1-3, 5-10, 12-15
X	IMMUNOTECHNOLOGY, vol. 2, no. 1, 1996, AMSTERDAM, NL, pages 47-57, XP002038653 N. MICHAEL ET AL.: "In vitro and in vivo characterization of a recombinant carboxypeptidase G2::anti-CEA scFv fusion protein." see the whole document	1-3, 5-10, 12-15
X	WO 96 11013 A (IMMUNOMEDICS) 18 April 1996 see examples see claims	1-5, 8-10, 12-15
X	CANCER RESEARCH, vol. 55, no. 23 suppl., 1 December 1995, BALTIMORE, MD, USA, pages 5968S-5972S, XP002038654 S. LEUNG ET AL.: "Bacterial expression of a kemptide fusion protein facilitates 32P labeling of a humanized, anti-carcinoembryonic antigen (hMN-14) antibody fragment." see abstract	1-5, 8-10, 12-15
X	WO 92 01059 A (CELLTECH LTD.) 23 January 1992 see examples see claims	1-4,8-10
X	CANCER RESEARCH, vol. 54, no. 7, 1 April 1994, BALTIMORE, MD, USA, pages 2151-2159, XP002038655 K. BOSSLET ET AL.: "Tumor-selective prodrug activation by fusion protein-mediated catalysis." see abstract	1-6, 12-15
A	WO 94 25585 A (GENPHARM INTERNATIONAL, INC.) 10 November 1994 see example 22 see claims	8-10,14

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

ernational application No.
PCT/GB 97/01165

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.: 15
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claim 15 is directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

2. [ ] Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [ ] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

...formation on patent family members

Inter... ...nal Application No
PCT/GB 97/01165

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
EP 633029 A	11-01-95	AT 119782 T	15-04-95
		CA 1336166 A	04-07-95
		DE 68921749 D	20-04-95
		DE 68921749 T	13-07-95
		EP 0414741 A	06-03-91
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		GB 2251859 A,B	22-07-92
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		CA 2161351 A	10-11-94
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